STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 156553

TO: Jegatheesan Seharaseyon Location: REM-4C61&4C70 Art Unit: 1647 Thursday, June 16, 2005 Case Serial Number: 09/920137	From: Alex Waclawiw Location: Biotech-Chem Library CM1-6A02 Phone: 308-4491 Alexandra.waclawiw@uspto.gov

Search Notes

This Page Blank (uspto)

STIC-Biotech/ChemLib 156553

From: Chan, Christina
Sent: Wednesday, June 15, 2005 2:29 PM
To: Seharaseyon, Jegatheesan; STIC-Biotech/ChemLib
Subject: RE: RE: Rush search

CRF

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----
From: Seharaseyon, Jegatheesan
Sent: Wednesday, June 15, 2005 9:25 AM
To: Chan, Christina
Subject: RE: Rush search
Importance: High

Hi,
Please rush search SEQ ID NO: 7 and 8 of 09/920137 in pending and commercial databases.

Thanks in advance,
Seyon.

J.Seharaseyon
Art Unit 1647
Remsen 4C61
Mailbox 4C70
Phone: (571)-272-0892
Fax: (571)-273-0892

****
STAFF USE ONLY
Searcher:_____
Searcher Phone: 2-
Date Searcher Picked up: 6-16-05
Date Completed: 6-16-05
Searcher Prep/Rev. Time: 10
Online Time: 10

Point of Contact:
Alexandra Waclawiw
Technical Info. Specialist
CM1 6A02 Tel: 308-4491

****
Type of Search
NA#:_____ AA#: 2
Interference:____ SPDI:___
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure#:_____ Text:___
Inventor:____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other(Specify):_____

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 07:35:00 ; Search time 115.516 Seconds
(without alignments)
509.793 Million cell updates/sec

Title: US-09-920-137D-7
Perfect score: 608
Sequence: 1 QVQLVESGGGVVQPGRSLRL.....CARDRGISAGGNYYYYGMDV 115

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	511	84.0	613	2	Q8WUK1	Q8wuk1 homo sapien
2	510	83.9	116	2	Q9UL93	Q9ul93 homo sapien
3	507.5	83.5	240	2	Q65ZC9	Q65zc9 homo sapien
4	495.5	81.5	122	1	HV3G_HUMAN	P01768 homo sapien
5	493	81.1	113	2	Q9UL90	Q9ul90 homo sapien
6	475	78.1	147	2	Q9Y509	Q9y509 homo sapien
7	474.5	78.0	472	2	Q6N089	Q6n089 homo sapien
8	470.5	77.4	478	2	Q6PI81	Q6pi81 homo sapien
9	470	77.3	597	2	Q96BB9	Q96bb9 homo sapien
10	469	77.1	121	1	HV3J_HUMAN	P01771 homo sapien
11	468.5	77.1	122	2	Q9UL84	Q9ul84 homo sapien
12	464	76.3	573	2	Q8WU38	Q8wu38 homo sapien
13	464	76.3	606	2	Q6GMY2	Q6gmy2 homo sapien
14	457.5	75.2	122	1	HV3H_HUMAN	P01769 homo sapien
15	456	75.0	119	1	HV3I_HUMAN	P01770 homo sapien
16	455	74.8	544	2	Q6PJ95	Q6pj95 homo sapien
17	450.5	74.1	126	1	HV3K_HUMAN	P01772 homo sapien
18	448.5	73.8	470	2	Q6PJA4	Q6pja4 homo sapien
19	448	73.7	121	2	Q9UL71	Q9ul71 homo sapien
20	442	72.7	117	1	HV3C_HUMAN	P01764 homo sapien
21	438	72.0	519	2	Q6N092	Q6n092 homo sapien
22	436.5	71.8	464	2	Q6MZU6	Q6mzu6 homo sapien
23	436	71.7	493	2	Q8NCL6	Q8ncl6 homo sapien
24	430	70.7	95	2	Q9ULB6	Q9ulb6 homo sapien
25	429	70.6	136	1	HV16_MOUSE	P01783 mus musculu
26	428	70.4	118	2	Q9UL91	Q9ul91 homo sapien
27	425	69.9	493	2	Q6GMX2	Q6gmx2 homo sapien
28	423.5	69.7	116	1	HV05_CARAU	P19181 carassius a
29	423	69.6	112	2	Q9HCC1	Q9hcc1 homo sapien
30	423	69.6	466	2	Q6IN78	Q6in78 homo sapien
31	422	69.4	120	1	HV3E_HUMAN	P01766 homo sapien
32	421.5	69.3	118	2	Q9UL72	Q9ul72 homo sapien
33	421.5	69.3	482	2	Q7Z351	Q7z351 homo sapien
34	421	69.2	119	1	HV3L_HUMAN	P01773 homo sapien
35	420	69.1	473	2	Q6MZV7	Q6mzv7 homo sapien
36	419	68.9	475	2	Q6MZQ6	Q6mzq6 homo sapien
37	417.5	68.7	116	1	HV3T_HUMAN	P01781 homo sapien
38	416	68.4	475	2	Q6GMW7	Q6gmw7 homo sapien
39	415.5	68.3	499	2	Q8N5K4	Q8n5k4 homo sapien
40	414.5	68.2	487	2	Q99KA4	Q99ka4 mus musculu
41	413.5	68.0	119	1	HV3M_HUMAN	P01774 homo sapien
42	411	67.6	487	2	Q6ZVX0	Q6zvx0 homo sapien
43	410.5	67.5	494	2	Q96K68	Q96k68 homo sapien
44	409	67.3	479	2	Q6MZV6	Q6mzv6 homo sapien
45	409	67.3	493	2	Q68CN4	Q68cn4 homo sapien
46	408.5	67.2	465	2	Q6P6C4	Q6p6c4 homo sapien
47	406	66.8	114	1	HV3B_HUMAN	P01763 homo sapien
48	406	66.8	485	2	Q6PDB8	Q6pdb8 mus musculu
49	404	66.4	119	2	Q920E7	Q920e7 mus musculu
50	404	66.4	480	2	Q6N094	Q6n094 homo sapien
51	403.5	66.4	115	1	HV3F_HUMAN	P01767 homo sapien
52	403	66.3	473	2	Q91Z05	Q91z05 mus musculu
53	400	65.8	196	2	Q65ZL8	Q65zl8 mus musculu
54	400	65.8	483	2	Q6MZX9	Q6mzx9 homo sapien
55	399	65.6	119	1	HV3N_HUMAN	P01775 homo sapien
56	395	65.0	255	2	Q6KB05	Q6kb05 mus musculu
57	394	64.8	98	1	HV57_MOUSE	P18528 mus musculu
58	393	64.6	117	1	HV54_MOUSE	P18525 mus musculu
59	392	64.5	117	1	HV3O_HUMAN	P01776 homo sapien
60	391	64.3	117	1	HV55_MOUSE	P18526 mus musculu
61	391	64.3	479	2	Q91WP5	Q91wp5 mus musculu
62	391	64.3	481	2	Q6N097	Q6n097 homo sapien
63	387.5	63.7	97	1	HV56_MOUSE	P18527 mus musculu
64	387	63.7	120	1	HV3U_HUMAN	P01782 homo sapien
65	384	63.2	248	2	Q65ZQ7	Q65zq7 mus sp. b3(
66	383	63.0	115	1	HV3D_HUMAN	P01765 homo sapien
67	380	62.5	117	1	HV03_CARAU	P19180 carassius a
68	379	62.3	466	2	Q6N096	Q6n096 homo sapien
69	378	62.2	494	2	Q6ZW64	Q6zw64 homo sapien
70	377	62.0	117	1	HV58_MOUSE	P18529 mus musculu
71	376	61.8	122	1	HV3A_HUMAN	P01762 homo sapien
72	375.5	61.8	470	2	Q7Z5W1	Q7z5w1 homo sapien
73	373	61.3	117	1	HV01_CAICR	P01813 caiman croc
74	371	61.0	119	1	HV3P_HUMAN	P01777 homo sapien
75	370.5	60.9	117	1	HV02_CANFA	P01785 canis famil
76	368.5	60.6	471	2	Q66K04	Q66k04 mus musculu
77	367.5	60.4	123	1	HV18_MOUSE	P01787 mus musculu
78	367.5	60.4	614	2	Q6DDQ7	Q6ddq7 xenopus lae
79	367	60.4	117	1	HV53_MOUSE	P18524 mus musculu
80	367	60.4	117	1	HV59_MOUSE	P18530 mus musculu
81	366.5	60.3	123	1	HV19_MOUSE	P01788 mus musculu
82	366.5	60.3	123	1	HV25_MOUSE	P01794 mus musculu
83	366	60.2	142	1	HV01_RAT	P01805 rattus norv
84	366	60.2	487	2	Q80ZI7	Q80zi7 mus musculu
85	365	60.0	593	2	Q6INM5	Q6inm5 xenopus lae
86	364.5	60.0	119	1	HV37_MOUSE	P01807 mus musculu
87	363	59.7	122	1	HV21_MOUSE	P01790 mus musculu
88	362.5	59.6	123	1	HV23_MOUSE	P01792 mus musculu
89	362	59.5	113	1	HV30_MOUSE	P01799 mus musculu
90	362	59.5	113	1	HV34_MOUSE	P01803 mus musculu
91	362	59.5	122	1	HV20_MOUSE	P01789 mus musculu
92	361	59.4	112	2	Q9UGP3	Q9ugp3 homo sapien
93	361	59.4	123	1	HV22_MOUSE	P01791 mus musculu
94	361	59.4	131	2	Q9UL88	Q9ul88 homo sapien
95	360.5	59.3	123	1	HV24_MOUSE	P01793 mus musculu
96	360.5	59.3	480	2	Q91XE1	Q91xe1 mus musculu
97	359.5	59.1	119	1	HV38_MOUSE	P01808 mus musculu
98	359.5	59.1	486	2	Q91Z07	Q91z07 mus musculu
99	358	58.9	114	1	HV01_CANFA	P01784 canis famil
100	358	58.9	115	1	HV32_MOUSE	P01801 mus musculu

ALIGNMENTS

```
RESULT 1
Q8WUK1
ID   Q8WUK1      PRELIMINARY;      PRT;   613 AA.
AC   Q8WUK1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHM protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC020240; AAH20240.1; -.
DR   PIR; F36005; F36005.
DR   PIR; G36005; G36005.
DR   PIR; PH1642; PH1642.
DR   PIR; PH1643; PH1643.
DR   PIR; PH1645; PH1645.
DR   PIR; PH1646; PH1646.
DR   PIR; PL0098; PL0098.
DR   PIR; PL0120; PL0120.
DR   PIR; S15590; S15590.
DR   PIR; S31116; S31116.
DR   PIR; S31119; S31119.
DR   PIR; S70442; S70442.
DR   HSSP; P01861; 1ADQ.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ   SEQUENCE   613 AA;  67295 MW;  60C7F5950671E315 CRC64;

  Query Match             84.0%;  Score 511;  DB 2;  Length 613;
  Best Local Similarity   98.0%;  Pred. No. 4.9e-44;
  Matches   97;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db         20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARD 99
              |||||||||||||||||||||||||||||||||||||:|
Db         80 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKD 118
```

```
RESULT 2
Q9UL93
ID   Q9UL93      PRELIMINARY;      PRT;   116 AA.
AC   Q9UL93;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035021; AAD56257.1; -.
DR   PIR; PH1644; PH1644.
DR   PIR; PL0120; PL0120.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12434 MW;  0DA0348154DD6061 CRC64;

  Query Match             83.9%;  Score 510;  DB 2;  Length 116;
  Best Local Similarity   89.2%;  Pred. No. 8.9e-45;
  Matches   99;  Conservative    3;  Mismatches    5;  Indels    4;  Gaps    1;

Qy          2 VQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYA 61
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYA 60

Qy         62 DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYG 112
              |||||||||||||||||||||||||||||:||||   |:  |    |:|
Db         61 DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAMYYCAGGGGLGLG----YWG 107
```

```
RESULT 3
Q65ZC9
ID   Q65ZC9      PRELIMINARY;      PRT;   240 AA.
AC   Q65ZC9;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Single-chain Fv (Fragment).
GN   Name=scFv;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C1q/7;
RX   MEDLINE=97362799; PubMed=9219263;
RA   Kontermann R.E., Wing M.G., Winter G.;
RT   "Complement recruitment using bispecific diabodies.";
RL   Nat. Biotechnol. 15:629-631(1997).
DR   EMBL; Y13056; CAA73499.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
```

```
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
FT   NON_TER      1      1
FT   NON_TER    240    240
SQ   SEQUENCE   240 AA;  25569 MW;  FDCFD3645F64B373 CRC64;

  Query Match             83.5%;  Score 507.5;  DB 2;  Length 240;
  Best Local Similarity   83.2%;  Pred. No. 3.8e-44;
  Matches   99;  Conservative    4;  Mismatches    3;  Indels   13;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||:||||:|||| |||||||||||||||| ||||||||||||||||||||||||||
Db          1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRG-------------ISAGG 106
              |||||||||||||||||||||||||||||||||||| |             :|:||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDWGDSLDPWGKGTLVTVSSGG 119


RESULT 4
HV3G_HUMAN
ID   HV3G_HUMAN     STANDARD;      PRT;   122 AA.
AC   P01768;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig heavy chain V-III region CAM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=81013859; PubMed=6774332;
RA   Lehman D.W., Putnam F.W.;
RT   "Amino acid sequence of the variable region of a human mu chain:
RT   location of a possible JH segment.";
RL   Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC   -!- MISCELLANEOUS: This mu chain was isolated from the plasma of a
CC       patient with macroglobulinemia.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02051; M3HUAM.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region;
KW   Pyrrolidone carboxylic acid.
FT   DOMAIN       1    112       Ig-like.
FT   MOD_RES      1      1       Pyrrolidone carboxylic acid.
FT   NON_TER    122    122
SQ   SEQUENCE   122 AA;  13668 MW;  A42D0F17D252F1C2 CRC64;

  Query Match             81.5%;  Score 495.5;  DB 1;  Length 122;
  Best Local Similarity   80.9%;  Pred. No. 3e-43;
  Matches   93;  Conservative   12;  Mismatches    5;  Indels    5;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||:|||||||||:|||||||||||||||:|||||||| ||||||||||||:| :|||
Db          1 QVELVESGGGVVZPGRSLRLSCAASGFTFSNYAMHWVRQPPGKGLEWVAVISYBGBBKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNY---YYYG 112
              |:||||||||||:||:||||||||||||:|||||||||| :   |:|    |:|
Db         61 ABSVKGRFTISRDBSKBTLYLQMNSLRAEBTAVYYCARDRPLY--GBYRAFNYWG 113


RESULT 5
```

```
Q9UL90
ID   Q9UL90      PRELIMINARY;      PRT;   113 AA.
AC   Q9UL90;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035024; AAD56260.1; -.
DR   PIR; S78486; S78486.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER      1      1
FT   NON_TER    113    113
SQ   SEQUENCE   113 AA;  12437 MW;  ED57FDD19086D07F CRC64;

  Query Match             81.1%;  Score 493;  DB 2;  Length 113;
  Best Local Similarity   85.7%;  Pred. No. 4.9e-43;
  Matches   96;  Conservative    3;  Mismatches    7;  Indels    6;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||||||||||||| |||||||||||||||| |||||||||||||| | ||||||||
Db          1 EVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIRYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYG 112
              |||||||||||||||||||||||||||||||||||:|       ||:  |
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDL------NYWGQG 106


RESULT 6
Q9Y509
ID   Q9Y509      PRELIMINARY;      PRT;   147 AA.
AC   Q9Y509;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VH3 protein (Fragment).
GN   Name=VH3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96071149; PubMed=7475288;
RA   Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA   Lichtenstein A.K., Berenson J.R.;
RT   "A CD10-positive subset of malignant cells is identified in multiple
RT   myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL   Leukemia 9:1948-1953(1995).
DR   EMBL; S80860; AAD14339.1; -.
DR   HSSP; P01842; 1AQK.
DR   GO; GO:0005887; C:integral to plasma membrane; NAS.
DR   GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
```

```
FT   NON_TER     147    147
SQ   SEQUENCE   147 AA;  15768 MW;  8489FCAAA7BC925C CRC64;

  Query Match             78.1%;  Score 475;  DB 2;  Length 147;
  Best Local Similarity   78.9%;  Pred. No. 4.8e-41;
  Matches   90;  Conservative    7;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              || |||||||||||:|||||| |||||||:| | ||||||||||:|||:|||||| :||
Db          1 QVHLVESGGGVVQPGKSLRLSCEASGFTFSTYGMSWVRQAPGKGLDWVALISYDGSTQYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMD 114
              | ||||||||||||||||||| ||| |||||||||:|       ||| |:|
Db         61 AGSVKGRFTISRDNSKNTLYLQMTSLRVEDTAVYYCAKDGNYFDSVGYYYAGID 114


RESULT 7
Q6N089
ID   Q6N089      PRELIMINARY;      PRT;   472 AA.
AC   Q6N089;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686P15220.
GN   Name=DKFZp686P15220;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human rectum tumor;
RG   The German Human cDNA Consortium;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640627; CAE45781.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   472 AA;  51724 MW;  26CB340D0046D279 CRC64;

  Query Match             78.0%;  Score 474.5;  DB 2;  Length 472;
  Best Local Similarity   78.3%;  Pred. No. 2.1e-40;
  Matches   90;  Conservative   11;  Mismatches   11;  Indels    3;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||||||||:|||||||||||||||  ||||||||||||||||: ||::  :  |
Db         20 EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIAY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||| ||:|||||||||||||:||||:: |     |:|||||||
Db         80 ADSVKGRFTISRDNGKNSLYLQMNSLRAEDTALYYCAKEIG---AHNFYYYGMDV 131


RESULT 8
Q6PI81
ID   Q6PI81      PRELIMINARY;      PRT;   478 AA.
AC   Q6PI81;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC041037; AAH41037.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   478 AA;  52666 MW;  17BED38D917970D6 CRC64;

  Query Match             77.4%;  Score 470.5;  DB 2;  Length 478;
  Best Local Similarity   78.0%;  Pred. No. 5.5e-40;
  Matches   92;  Conservative    8;  Mismatches   15;  Indels    3;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||||||||:|||| |||||||||||||||| | |||||||||||||  |  ||| |||
Db         20 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARD---RGISAGGNYYYYGMDV 115
              |||||||||||||:||:|||||||||||||||||||:      :   :|||: |||
Db         80 VDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREFESTMTTVNADYYYFYMDV 137


RESULT 9
Q96BB9
ID   Q96BB9      PRELIMINARY;      PRT;   597 AA.
AC   Q96BB9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHM protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC015760; AAH15760.1; -.
DR   PIR; S05271; S05271.
DR   PIR; S24260; S24260.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ   SEQUENCE   597 AA;  65039 MW;  4FCA3AD8ECE263D9 CRC64;

  Query Match             77.3%;  Score 470;  DB 2;  Length 597;
  Best Local Similarity   79.3%;  Pred. No. 8e-40;
  Matches   92;  Conservative   11;  Mismatches    9;  Indels    4;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||:|||||:|||| ||||||||||:||||||:||||||||||||: ||  | : ||
Db         20 EVQLLESGGGLVQPGGSLRLSCAASGFSFSSYAMNWVRQAPGKGLEWVSAISGSGGSTYY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARD-RGISAGGNYY---YYG 112
              ||||||||||||||::|||||||||||||||||||:| || || |||    |:|
Db         80 ADSVKGRFTISRDNSRDTLYLQMNSLRAEDTAVYYCAKDPRGYSASGNYTREDYWG 135


RESULT 10
HV3J_HUMAN
ID   HV3J_HUMAN     STANDARD;      PRT;   121 AA.
AC   P01771;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig heavy chain V-III region HIL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=79124695; PubMed=420800;
RA   Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
RT   "Amino acid sequence of the VH region of human myeloma
RT   cryoimmunoglobulin IgG Hil.";
RL   Biochemistry 18:553-560(1979).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
CC       protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02054; G1HUHL.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region;
KW   Pyrrolidone carboxylic acid.
FT   DOMAIN        1    112       Ig-like.
FT   MOD_RES       1      1       Pyrrolidone carboxylic acid.
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  13566 MW;  480FC53610EF5DAB CRC64;

  Query Match             77.1%;  Score 469;  DB 1;  Length 121;
  Best Local Similarity   76.5%;  Pred. No. 1.6e-40;
  Matches   88;  Conservative   10;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||:||::|||||||||||||| |||||||:| |||||||||||||||||| |:||  ||
Db          1 QVKLVQAGGGVVQPGRSLRLSCIASGFTFSNYGMHWVRQAPGKGLEWVAVIWYNGSRTYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              ||||||||||||||| |||::|||||  |||||||||||  |    :: |:|  |
Db         61 GDSVKGRFTISRDNSKRTLYMZMNSLRTEDTAVYYCARDPDILTAFSFDYWGQGV 115


RESULT 11
Q9UL84
ID   Q9UL84      PRELIMINARY;      PRT;   122 AA.
AC   Q9UL84;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035030; AAD56266.1; -.
DR   HSSP; P01772; 2FB4.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  13579 MW;  36054D41366545B8 CRC64;

  Query Match             77.1%;  Score 468.5;  DB 2;  Length 122;
  Best Local Similarity   81.4%;  Pred. No. 1.8e-40;
  Matches   92;  Conservative    7;  Mismatches   13;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||||||||||||||||||||| |||||:| |||||||||||||| || |||||:|
```

```
Db          1 EVQLVESGGGVVQPGRSLRLSCAASRFTFSNYGMHWVRQAPGKGLEWVAAISNDGSNKFY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARD-RGISAGGNYYYYG 112
              |||||||||| |||||| : |||||||||||||||||:| ||    |  : |:|
Db         61 ADSVKGRFTIFRDNSKNMMDLQMNSLRAEDTAVYYCAKDERGRLVGTYFDYWG 113


RESULT 12
Q8WU38
ID   Q8WU38      PRELIMINARY;      PRT;   573 AA.
AC   Q8WU38;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC021276; AAH21276.1; -.
DR   PIR; S21205; S21205.
DR   PIR; S30532; S30532.
DR   HSSP; P18529; 1I8K.
DR   Pfam; PF07654; C1-set; 2.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   573 AA;  62967 MW;  FD072344033AC530 CRC64;

  Query Match            76.3%;  Score 464;  DB 2;  Length 573;
  Best Local Similarity  76.9%;  Pred. No. 3.2e-39;
  Matches   90;  Conservative   11;  Mismatches   10;  Indels    6;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||||||||:|||||||||||||||||  |||||||||||||||: ||::  :  |
Db         20 EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNY--YYYGMDV 115
              |||||||||||||:||:|||||||||||||:||||:       |:|  |||||||
Db         80 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAK----HGSGSYIGYYYGMDV 132
```

```
RESULT 13
Q6GMY2
ID   Q6GMY2      PRELIMINARY;      PRT;   606 AA.
AC   Q6GMY2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073758; AAH73758.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW   Hypothetical protein.
SQ   SEQUENCE   606 AA;  66184 MW;  B6B38B51114E4C55 CRC64;

  Query Match            76.3%;  Score 464;  DB 2;  Length 606;
  Best Local Similarity  75.6%;  Pred. No. 3.4e-39;
  Matches   93;  Conservative    7;  Mismatches   15;  Indels    8;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||:|:|| |||||||||||||| | | |:|||||||||||: ||   |   |
Db         20 QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSSSYTNY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR-DRGISAGGN-------YYYYG 112
              |||||||||||||:||:|||||||||||||||||||||   ||:| |        |||||
Db         80 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGGNGIAAAGRVVYAEDYYYYYG 139

Qy        113 MDV 115
              |||
Db        140 MDV 142
```

```
RESULT 14
HV3H_HUMAN
ID   HV3H_HUMAN     STANDARD;      PRT;   122 AA.
AC   P01769;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig heavy chain V-III region GA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=74175307; PubMed=4208843;
RA   Florent G., Lehman D., Putnam F.W.;
RT   "The switch point in mu heavy chains of human IgM immunoglobulins.";
RL   Biochemistry 13:2482-2498(1974).
CC   -!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
CC       macroglobulin.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02052; M3HUGA.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region;
KW   Pyrrolidone carboxylic acid.
FT   DOMAIN        1    112       Ig-like.
FT   MOD_RES       1      1       Pyrrolidone carboxylic acid.
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  13166 MW;  74E5B6959E84100A CRC64;

  Query Match             75.2%;  Score 457.5;  DB 1;  Length 122;
  Best Local Similarity   72.2%;  Pred. No. 2.5e-39;
  Matches   83;  Conservative   19;  Mismatches   10;  Indels    3;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||:||:|||| |:|||||||||||||:||:|||||||||||||:|::||||:| ::||
Db          1 QVZLVZSGGGAVZPGRSLRLSCAASGFSFSTYAMHWVRQAPGKGLZWLSVISYBGBBZYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARD---RGISAGGNYYYYG 112
                |||||||||::||:|:||:||||||||:||||||||      |  || :|:  |
Db         61 AASVKGRFTISRBBSKBTMYLEMNSLRAENTAVYYCARSGIALGSVAGTDYWGZG 115


RESULT 15
HV3I_HUMAN
ID   HV3I_HUMAN     STANDARD;      PRT;   119 AA.
AC   P01770;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig heavy chain V-III region NIE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77070269; PubMed=826475;
RA   Ponstingl H., Hilschmann N.;
RT   "The rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic
RT   peptides of the H-chain, alignment of the tryptic peptides and
RT   discussion of the complete structure.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN   [2]
RP   DISULFIDE BOND.
RX   MEDLINE=77070267; PubMed=1002129;
RA   Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie), I: purification and
RT   characterization of the protein, the L- and H-chains, the cyanogen
RT   bromide cleavage products, and the disulfide bridges.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
CC       protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A91668; G1HUNI.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region;
KW   Pyrrolidone carboxylic acid.
FT   DOMAIN        1    112       Ig-like.
FT   MOD_RES       1      1       Pyrrolidone carboxylic acid.
FT   DISULFID     22     96
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13242 MW;  C96935A6E55E165B CRC64;

  Query Match             75.0%;  Score 456;  DB 1;  Length 119;
  Best Local Similarity   85.0%;  Pred. No. 3.4e-39;
  Matches   85;  Conservative    8;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||:|||||||||||||||||||||||| | :|||||||||||||||:||:| :|:|
Db          1 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSRYTIHWVRQAPGKGLEWVAVMSYBGBBKHY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR 100
              |||| |||||||::||||||| ||||| |||||||||| |
Db         61 ADSVNGRFTISRNDSKNTLYLNMNSLRPEDTAVYYCARIR 100


RESULT 16
Q6PJ95
ID   Q6PJ95       PRELIMINARY;      PRT;   544 AA.
AC   Q6PJ95;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
```

```
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019046; AAH19046.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   544 AA;  60102 MW;  1895814B2297C668 CRC64;

  Query Match             74.8%;  Score 455;  DB 2;  Length 544;
  Best Local Similarity   87.0%;  Pred. No. 2.5e-38;
  Matches   87;  Conservative    4;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              | |||||||||||||| |||||||||||  ||:| ||||||||||||||||||  ||| |:|||
Db         20 QAQLVESGGGVVQPGSSLRLSCAASGFRFSNYGMHWVRQAPGKGLEWVAVFSYDESDKYY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR 100
              | ||||||||||||||||| ||||||| |||||||||:|:
Db         80 AASVKGRFTISRDNSKNTLSLQMNSLRVEDTAVYYCAKDQ 119


RESULT 17
HV3K_HUMAN
ID   HV3K_HUMAN     STANDARD;      PRT;   126 AA.
AC   P01772;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig heavy chain V-III region KOL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE, AND DISULFIDE BONDS.
RX   MEDLINE=83289131; PubMed=6884994;
RA   Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT   "Three-dimensional structure determination of antibodies. Primary
RT   structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=81072295; PubMed=7441755;
RA   Marquart M., Deisenhofer J., Huber R., Palm W.;
RT   "Crystallographic refinement and atomic models of the intact
RT   immunoglobulin molecule Kol and its antigen-binding fragment at 3.0 A
RT   and 1.0-A resolution.";
RL   J. Mol. Biol. 141:369-391(1980).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A02055; G1HUKL.
DR   PDB; 2FB4; X-ray; H=1-126.
DR   PDB; 2IG2; X-ray; H=-.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Direct protein sequencing; Immunoglobulin V region;
KW   Pyrrolidone carboxylic acid.
FT   DOMAIN       1    112       Ig-like.
FT   MOD_RES      1      1       Pyrrolidone carboxylic acid.
FT   DISULFID    22     96
FT   DISULFID   105    110
FT   STRAND       3      7
FT   STRAND      11     12
FT   TURN        14     15
FT   STRAND      18     25
FT   HELIX       29     31
FT   STRAND      34     39
FT   TURN        41     42
FT   STRAND      45     51
FT   TURN        53     54
FT   STRAND      58     60
FT   HELIX       62     64
FT   STRAND      65     65
FT   TURN        66     67
FT   STRAND      68     73
FT   TURN        74     77
FT   STRAND      78     83
FT   HELIX       88     90
FT   STRAND      92     99
FT   STRAND     106    106
FT   TURN       107    108
FT   STRAND     109    109
FT   STRAND     113    116
FT   STRAND     120    124
FT   NON_TER    126    126
SQ   SEQUENCE   126 AA;  13718 MW;  E4D71B52B16F8776 CRC64;

  Query Match             74.1%;  Score 450.5;  DB 1;  Length 126;
  Best Local Similarity   74.6%;  Pred. No. 1.3e-38;
  Matches   91;  Conservative   12;  Mismatches   12;  Indels    7;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||||||||||||::||| |||||:|||||||||||||:|  |||:::|
Db          1 QVQLVESGGGVVQPGRSLRLSCSSSGFIFSSYAMYWVRQAPGKGLEWVAIIWDDGSDQHY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRG----ISA---GGNYYYYGM 113
              ||||||||||||||||:|||:||| ||| ||:|||| |     ||   | :|:  |
Db         61 ADSVKGRFTISRDNSKNTLFLQMDSLRPEDTGVYFCARDGGHGFCSSASCFGPDYWGQGT 120

Qy        114 DV 115
              ||
Db        121 PV 122


RESULT 18
Q6PJA4
ID   Q6PJA4      PRELIMINARY;      PRT;   470 AA.
AC   Q6PJA4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
```

```
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018747; AAH18747.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51715 MW;  7B49556A11FD7D99 CRC64;

  Query Match             73.8%;  Score 448.5;  DB 2;  Length 470;
  Best Local Similarity   79.8%;  Pred. No. 1e-37;
  Matches   87;  Conservative    6;  Mismatches   11;  Indels    5;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||||||||:|||| ||||||  |||||||| | |||||||||||||| |  ||| |||
Db         20 EVQLVESGGGLVQPGGSLRLSCVVSGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYY 109
                ||||||||||||:||:||||||||||||||||||     | ::|
Db         80 VDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARD-----GSSWY 123


RESULT 19
Q9UL71
ID   Q9UL71      PRELIMINARY;      PRT;   121 AA.
AC   Q9UL71;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035043; AAD56279.1; -.
DR   HSSP; P01852; 1NFD.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  13154 MW;  2F045CCFA5D50736 CRC64;

  Query Match             73.7%;  Score 448;  DB 2;  Length 121;
  Best Local Similarity   84.0%;  Pred. No. 2.3e-38;
  Matches   84;  Conservative    8;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||||||||||||| |||| ||||||||  ||||||||||||||||::|| || : ||
Db          1 EVQLVESGGGVVQPGGSLRLFCAASGFTFDGYAMHWVRQAPGKGLEWVSLISGDGGSTYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR 100
              ||||||||||||||||:|||||||||||||:||||: :
Db         61 ADSVKGRFTISRDNSKNSLYLQMNSLRAEDTALYYCAKGK 100


RESULT 20
HV3C_HUMAN
ID   HV3C_HUMAN     STANDARD;      PRT;   117 AA.
AC   P01764;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig heavy chain V-III region VH26 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81101090; PubMed=6450418;
RA   Matthyssens G., Rabbitts T.H.;
RT   "Structure and multiplicity of genes for the human immunoglobulin
RT   heavy chain variable region.";
RL   Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; J00236; AAA53516.1; -.
DR   EMBL; M35415; AAA58735.1; -.
DR   PIR; A02047; H3HU26.
DR   PDB; 1HOU; Model; H=20-117.
DR   Genew; HGNC:5545; IGHV@.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       Ig heavy chain V-III region VH26.
FT   DOMAIN       20   >117       Ig-like.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12582 MW;  E826733F1A3CB0F1 CRC64;

  Query Match             72.7%;  Score 442;  DB 1;  Length 117;
```

```
  Best Local Similarity   85.7%;  Pred. No. 9.3e-38;
  Matches   84;  Conservative    6;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||:|||||:|||| |||||||||||||||| ||||||||||||: ||  | : ||
Db         20 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR 98
               |||||||||||||||||||||||||||||||||||:
Db         80 GDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK 117


RESULT 21
Q6N092
ID   Q6N092      PRELIMINARY;      PRT;   519 AA.
AC   Q6N092;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686K18196 (Fragment).
GN   Name=DKFZp686K18196;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human esophagus tumor;
RG   The German Human cDNA Consortium;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640624; CAE45778.1; -.
DR   HSSP; P01842; 1AQK.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 4.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
FT   NON_TER       1       1
SQ   SEQUENCE   519 AA;  56423 MW;  F839EE7F811EB88D CRC64;

  Query Match             72.0%;  Score 438;  DB 2;  Length 519;
  Best Local Similarity   80.2%;  Pred. No. 1.4e-36;
  Matches   81;  Conservative    9;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              || |||||||||||||||||||| ||||  ::|||||||:||||:|:  :|||| ||
Db         44 QVHLVESGGGVVQPGRSLRLSCAAFGFTFGDHSMHWVRQAPGRGLEWMALTWFDGSNNYY 103

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRG 101
               ||||||||||||| :| ||||:| || ||||||||||:||
Db        104 ADSVKGRFTISRDNIRNILYLQINRLRDEDTAVYYCARERG 144


RESULT 22
Q6MZU6
ID   Q6MZU6      PRELIMINARY;      PRT;   464 AA.
AC   Q6MZU6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686C15213.
GN   Name=DKFZp686C15213;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Human rectum tumor;
RG   The German Human cDNA Consortium;
RA   Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640874; CAE45931.1; -.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   464 AA;  51099 MW;  2FCA72C66E8A0ABC CRC64;

  Query Match             71.8%;  Score 436.5;  DB 2;  Length 464;
  Best Local Similarity   74.8%;  Pred. No. 1.7e-36;
  Matches   86;  Conservative   13;  Mismatches    7;  Indels    9;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVI-SYDGSNKY 59
              :|||||||||:|:|| |||||||||||||||:|:|||||||||||:   | || :|
Db         20 EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSFSSRGGSYEY 79

Qy         60 YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMD 114
              ||||||||||||||:||:|||||||||||:||||||||| |       ::|:|
Db         80 YADSVKGRFTISRDNAKNSLYLQMNSLRAENTAVYYCARDLG--------WFGLD 126


RESULT 23
Q8NCL6
ID   Q8NCL6      PRELIMINARY;      PRT;   493 AA.
AC   Q8NCL6;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein FLJ90170.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Mammary gland;
RA   Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA   Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA   Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA   Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK074651; BAC11114.1; -.
DR   HSSP; P01876; 1OW0.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   493 AA;  53224 MW;  12ECD7E094777101 CRC64;

  Query Match             71.7%;  Score 436;  DB 2;  Length 493;
```

```
  Best Local Similarity   73.2%;  Pred. No. 2.1e-36;
  Matches   82;  Conservative   12;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||| || |||||||||| |  | ||||||:||:||||||:| |||:  ||
Db         20 QVQLVESGGGVVLPGGSLRLSCAASGFRFRDYDMHWVRQSPGEGLEWVALIWYDGTKTYY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYG 112
              :|||||| |:|||| ||||||:| || ||||||||||||:| :  | : ::|
Db         80 SDSVKGRLTVSRDNYKNTLYLEMKSLGAEDTAVYYCARDQGYAGYGVFDHWG 131


RESULT 24
Q9ULB6
ID   Q9ULB6      PRELIMINARY;      PRT;    95 AA.
AC   Q9ULB6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Imunoglobulin heavy chain (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Tange Y., Kayano H.;
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB035268; BAA87067.1; -.
DR   PIR; PH0872; PH0872.
DR   PIR; S36280; S36280.
DR   HSSP; P01820; 1G7J.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER      95     95
SQ   SEQUENCE   95 AA;  10527 MW;  90A8C6D16D22574A CRC64;

  Query Match             70.7%;  Score 430;  DB 2;  Length 95;
  Best Local Similarity   87.4%;  Pred. No. 1.3e-36;
  Matches   83;  Conservative    3;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          2 VQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYA 61
              ||| |||||:|||| |||||||||||||||| | |||||||||||||  ||| |||
Db          1 VQLEESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYV 60

Qy         62 DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC 96
              |||||||||||||:||:||||||||||||||||||
Db         61 DSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYC 95


RESULT 25
HV16_MOUSE
ID   HV16_MOUSE     STANDARD;      PRT;   136 AA.
AC   P01783;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig heavy chain V region MOPC 21 precursor (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
RN   [2]
RP   SEQUENCE OF 17-136.
RX   MEDLINE=77100368; PubMed=401950;
RA   Adetugbo K., Milstein C., Secher D.S.;
RT   "Molecular analysis of spontaneous somatic mutants.";
RL   Nature 265:299-304(1977).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00522; AAD15290.1; -.
DR   PIR; E90809; G1MS21.
DR   PDB; 1IGC; X-ray; H=-.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Direct protein sequencing; Immunoglobulin V region;
KW   Signal.
FT   NON_TER       1      1
FT   SIGNAL       <1     16
FT   CHAIN        17    136       Ig heavy chain V region MOPC 21.
FT   DOMAIN      115    119       D segment.
FT   DOMAIN      120    136       JH4 segment.
FT   DISULFID     38    112
FT   CONFLICT     75     78       HYAD -> DYAH (in Ref. 2).
FT   CONFLICT     89     90       DN -> ND (in Ref. 2).
FT   CONFLICT    115    115       W -> H (in Ref. 2).
FT   CONFLICT    120    120       Y -> W (in Ref. 2).
FT   STRAND       19     23
FT   STRAND       26     28
FT   TURN         30     31
FT   STRAND       34     41
FT   HELIX        45     47
FT   STRAND       50     55
FT   STRAND       61     67
FT   TURN         69     70
FT   STRAND       74     76
FT   HELIX        78     80
FT   STRAND       81     81
FT   TURN         82     83
FT   STRAND       84     89
FT   TURN         90     93
FT   STRAND       94     99
FT   HELIX       104    106
FT   STRAND      108    114
FT   TURN        118    119
FT   STRAND      125    126
FT   STRAND      130    134
FT   NON_TER     136    136
SQ   SEQUENCE   136 AA;  15071 MW;  2276A98DBDBF7016 CRC64;

  Query Match             70.6%;  Score 429;  DB 1;  Length 136;
  Best Local Similarity   74.3%;  Pred. No. 2.4e-36;
  Matches   84;  Conservative    8;  Mismatches   15;  Indels    6;  Gaps    1;

Qy          2 VQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYA 61
              |||||||||:|||| | :|||||||||||: |||||||| |||||||  |   :||
Db         18 VQLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTLHYA 77

Qy         62 DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMD 114
              |:|||||||||| ||||:||| |||:||||:|||||       ||| || ||
Db         78 DTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCAR------WGNYPYYAMD 124


Search completed: June 16, 2005, 07:38:55
Job time : 118.516 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 07:35:01 ; Search time 24.2377 Seconds
(without alignments)
456.518 Million cell updates/sec

Title: US-09-920-137D-7
Perfect score: 608
Sequence: 1 QVQLVESGGGVVQPGRSLRL.....CARDRGISAGGNYYYYGMDV 115

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	549	90.3	122	2	E36005	Ig heavy chain V r
2	547	90.0	128	2	S48797	Ig heavy chain V r
3	536.5	88.2	123	2	S38493	Ig heavy chain - h
4	528	86.8	133	2	A49028	Ig heavy chain V-I
5	525	86.3	121	2	G36005	Ig heavy chain V r
6	524	86.2	119	2	F36005	Ig heavy chain V r
7	519	85.4	121	2	S19666	Ig heavy chain V r
8	519	85.4	134	2	S31679	Ig heavy chain V r
9	518.5	85.3	114	2	S46390	Ig heavy chain V r
10	514	84.5	118	2	S31116	Ig heavy chain - h
11	513.5	84.5	122	2	S31119	Ig heavy chain - h
12	512.5	84.3	114	2	S46392	Ig heavy chain V r
13	512	84.2	98	2	S29546	Ig heavy chain V r
14	512	84.2	119	2	S31111	Ig heavy chain - h
15	511.5	84.1	132	2	S31603	Ig heavy chain V r
16	508.5	83.6	117	2	S36270	Ig heavy chain V r
17	508	83.6	130	2	PL0098	Ig heavy chain pre
18	507	83.4	120	2	S31112	Ig heavy chain - h
19	507	83.4	122	2	S31117	Ig heavy chain - h
20	505	83.1	98	2	PL0116	Ig heavy chain V-I
21	505	83.1	113	2	S38490	Ig heavy chain - h
22	504.5	83.0	117	2	S36259	Ig heavy chain V r
23	502.5	82.6	140	2	S70442	Ig heavy chain pre
24	499	82.1	137	2	S31701	Ig heavy chain V r
25	498	81.9	147	2	I37780	Ig variable region
26	497	81.7	130	2	S31601	Ig heavy chain V r
27	496	81.6	139	2	S31674	Ig heavy chain V r
28	495.5	81.5	122	1	M3HUAM	Ig heavy chain V-I
29	491.5	80.8	133	2	S31510	Ig heavy chain - h
30	489.5	80.5	115	2	S36284	Ig heavy chain V r
31	489	80.4	97	2	S44115	Ig heavy chain V r
32	489	80.4	114	2	S46391	Ig heavy chain V r
33	488	80.3	98	2	S29543	Ig heavy chain V r
34	488	80.3	111	2	PH1645	Ig heavy chain V r
35	488	80.3	134	2	S31688	Ig heavy chain V r
36	488	80.3	135	2	S31598	Ig heavy chain V r
37	487	80.1	94	2	PL0120	Ig heavy chain V-I
38	487	80.1	109	2	PH1644	Ig heavy chain V r
39	481	79.1	109	2	PH1646	Ig heavy chain V r
40	480.5	79.0	125	2	S37455	Ig mu chain - huma
41	480.5	79.0	160	2	S05271	Ig heavy chain pre
42	478.5	78.7	133	2	S31590	Ig heavy chain V r
43	475	78.1	111	2	PH1643	Ig heavy chain V r
44	474	78.0	118	2	PH1660	Ig heavy chain V r
45	471.5	77.5	151	2	A60943	Ig heavy chain pre
46	470	77.3	108	2	PH1642	Ig heavy chain V r
47	470	77.3	119	2	C36005	Ig heavy chain V r
48	470	77.3	120	2	S48798	Ig heavy chain V r
49	469	77.1	121	1	G1HUHL	Ig heavy chain V-I
50	468	77.0	119	2	S31107	Ig heavy chain - h
51	468	77.0	119	2	S31108	Ig heavy chain - h
52	467	76.8	118	2	PH1662	Ig heavy chain V r
53	466.5	76.7	122	2	S69910	Ig V-D-J region (K
54	466.5	76.7	127	2	S38489	Ig heavy chain - h
55	465	76.5	118	2	S31677	Ig heavy chain V r
56	461.5	75.9	120	2	S44111	Ig heavy chain V-D
57	461	75.8	125	2	S30531	Ig heavy chain V r
58	460.5	75.7	101	2	JT0511	Ig heavy chain V-I
59	460	75.7	114	2	S36280	Ig heavy chain V r
60	459.5	75.6	140	2	S31588	Ig heavy chain V r
61	457.5	75.2	121	2	PH1661	Ig heavy chain V r
62	457.5	75.2	122	1	M3HUGA	Ig heavy chain V-I
63	456	75.0	119	1	G1HUNI	Ig heavy chain V-I
64	454.5	74.8	123	2	S26794	Ig heavy chain V r
65	454.5	74.8	138	2	S31666	Ig heavy chain V r
66	454	74.7	121	2	S31113	Ig heavy chain - h
67	454	74.7	138	2	B56701	Ig heavy chain V r
68	453	74.5	117	2	S78486	Ig heavy chain V r
69	453	74.5	120	2	S36273	Ig heavy chain V r
70	452	74.3	115	2	S57445	Ig heavy chain V-J
71	452	74.3	139	2	I37781	Ig variable region
72	452	74.3	145	2	S11239	Ig heavy chain V r
73	451.5	74.3	124	2	S20782	Ig heavy chain V r
74	451	74.2	118	2	S31121	Ig heavy chain - h
75	451	74.2	120	2	S36278	Ig heavy chain V r
76	450.5	74.1	126	1	G1HUKL	Ig heavy chain V-I
77	449	73.8	98	2	S54856	Ig heavy chain V r
78	448	73.7	110	2	PH1655	Ig heavy chain V r
79	448	73.7	119	2	S37453	Ig mu chain - huma
80	448	73.7	140	2	S31686	Ig heavy chain V r
81	447.5	73.6	128	2	S26790	Ig heavy chain V r
82	447	73.5	97	2	PH0872	Ig heavy chain V r
83	447	73.5	98	2	PL0123	Ig heavy chain V-I
84	447	73.5	117	2	S17079	Ig heavy chain V-g
85	447	73.5	120	2	E49590	Ig heavy chain V r
86	447	73.5	136	2	S31587	Ig heavy chain V r
87	446	73.4	98	2	S26889	Ig heavy chain V r
88	446	73.4	117	2	A45953	Ig heavy chain pre
89	446	73.4	119	2	D36005	Ig heavy chain V r
90	446	73.4	123	2	S31114	Ig heavy chain - h
91	445	73.2	249	2	S69340	Ig heavy chain VHI
92	444.5	73.1	116	2	S31110	Ig heavy chain - h
93	444	73.0	143	2	S23624	Ig heavy chain V r
94	443	72.9	98	2	S26891	Ig heavy chain V r
95	443	72.9	110	2	S69897	Ig heavy chain V r
96	443	72.9	121	2	S31104	Ig heavy chain (su
97	443	72.9	122	2	S31675	Ig heavy chain V r
98	443	72.9	141	2	S31669	Ig heavy chain V r
99	442.5	72.8	114	2	S31120	Ig heavy chain - h
100	442	72.7	117	1	H3HU26	Ig heavy chain pre

ALIGNMENTS

RESULT 1
E36005
Ig heavy chain V region (M72) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C;Accession: E36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: E36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-122 <SCH>
A;Cross-references: GB:M34030
C;Genetics:
A;Gene: GDB:IGH@; IGHDY1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 90.3%; Score 549; DB 2; Length 122;
Best Local Similarity 93.0%; Pred. No. 4.4e-43;
Matches 107; Conservative 2; Mismatches 2; Indels 4; Gaps 1;

```
Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||  |:    :||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRHSSS----WYYGMDV 111
```

RESULT 2
S48797
Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999
C;Accession: S48797; S26893
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
A;Accession: S48797
A;Molecule type: mRNA
A;Residues: 1-128 <MAH>
A;Cross-references: EMBL:Z46379; NID:g587147; PIDN:CAA86512.1; PID:g1340168
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26893
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12350; NID:g32922; PIDN:CAA78220.1; PID:g32923
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 90.0%; Score 547; DB 2; Length 128;
Best Local Similarity 91.5%; Pred. No. 7e-43;
Matches 107; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

```
Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||||||||||||||||||||| |||||||||||||||| ||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGI--SAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||||||||||      |:|  ||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDNYYYDSSGYYYYYYGMDV 117
```

RESULT 3
S38493
Ig heavy chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S38493
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.
submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a ph
A;Reference number: S38488
A;Accession: S38493
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-123 <MAR>
A;Cross-references: EMBL:Z23036; NID:g414033; PIDN:CAA80571.1; PID:g414034
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 88.2%; Score 536.5; DB 2; Length 123;
Best Local Similarity 91.3%; Pred. No. 6.1e-42;
Matches 105; Conservative 1; Mismatches 6; Indels 3; Gaps 1;

```
Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||| |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQESGGGVVQPGRSLSLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||| |   :  ||||| |||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARAR---SNWNYYYYYMDV 112
```

RESULT 4
A49028
Ig heavy chain V-III region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: A49028
R;Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuurm
Eur. J. Immunol. 21, 2355-2363, 1991
A;Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphobl
A;Reference number: A49028; MUID:92008140; PMID:1915549
A;Accession: A49028
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-133 <TIM>
A;Cross-references: GB:S64471; NID:g236904; PIDN:AAB20011.1; PID:g236905
A;Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines
A;Note: sequence extracted from NCBI backbone (NCBIN:64471, NCBIP:64470)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.8%; Score 528; DB 2; Length 133;
Best Local Similarity 90.4%; Pred. No. 3.9e-41;
Matches 103; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

```
Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||||||||||||||||||| |||| ||||||||||||| ||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVLQAPGKGLEWVAVIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR--GISAGGNYYYYG 112
              |||||||||||||||||||||||||||||||||||||||||    |:| ||: |:|
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRRLTIAAAGNFDYWG 114
```

RESULT 5
G36005

```
Ig heavy chain V region (M74) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
C;Accession: G36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: G36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-121 <SCH>
A;Cross-references: UNIPROT:Q8WUK1; GB:M34031
C;Genetics:
A;Gene: GDB:IGH@; IGHDY1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             86.3%;  Score 525;  DB 2;  Length 121;
  Best Local Similarity   91.1%;  Pred. No. 6.6e-41;
  Matches  102;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYG 112
              |||||||||||||||||||||||||||||||||||||||       : |:|
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRKDWGWALFDYWG 112


RESULT 6
F36005
Ig heavy chain V region (M49) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
C;Accession: F36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: F36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <SCH>
A;Cross-references: UNIPROT:Q8WUK1; GB:M34026
C;Genetics:
A;Gene: GDB:IGH@; IGHDY1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             86.2%;  Score 524;  DB 2;  Length 119;
  Best Local Similarity   98.1%;  Pred. No. 8.1e-41;
  Matches  101;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGIS 103
              |||||||||||||||||||||||||||||||||||||||||||  |
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRKAS 103


RESULT 7
S19666
Ig heavy chain V region (VH3DJH4) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19666
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on pha
A;Reference number: S19663; MUID:92085276; PMID:1748994
A;Accession: S19666
A;Molecule type: mRNA
A;Residues: 1-121 <MAR>
A;Cross-references: EMBL:X61646; NID:g37688; PIDN:CAA43827.1; PID:g1335369
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             85.4%;  Score 519;  DB 2;  Length 121;
  Best Local Similarity   89.4%;  Pred. No. 2.3e-40;
  Matches  101;  Conservative    5;  Mismatches    5;  Indels    2;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||:|||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          1 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYY-YYG 112
              |||||||||||||||||||||||||||||||||||||:  | |:|  |: |:|
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK-TGYSSGWGYFDYWG 112


RESULT 8
S31679
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31679
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31679
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-134 <CUI>
A;Cross-references: EMBL:Z14203; NID:g30965; PIDN:CAA78572.1; PID:g30966
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

  Query Match             85.4%;  Score 519;  DB 2;  Length 134;
  Best Local Similarity   90.2%;  Pred. No. 2.6e-40;
  Matches  101;  Conservative    4;  Mismatches    3;  Indels    4;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYG 112
              |||||||||||||||||||||||||||||||||||:    : |:|:  |
Db         80 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARE----SRGDYWGQG 127


RESULT 9
S46390
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46390
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A;Reference number: S46390; MUID:94254092; PMID:8196048
A;Accession: S46390
A;Status: preliminary
A;Molecule type: DNA
```

```
A;Residues: 1-114 <FIG>
A;Cross-references: EMBL:Z31686; NID:g509782; PIDN:CAA83491.1; PID:g1335143
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             85.3%;  Score 518.5;  DB 2;  Length 114;
  Best Local Similarity   90.2%;  Pred. No. 2.4e-40;
  Matches  101;  Conservative    3;  Mismatches    3;  Indels    5;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYG 112
              ||||||||||||||||||||||||||||||||||||      |:|:  |
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARD-----WGDYWGQG 107


RESULT 10
S31116
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S31116
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31116
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-118 <RAA>
A;Cross-references: UNIPROT:Q8WUK1; EMBL:X62966
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             84.5%;  Score 514;  DB 2;  Length 118;
  Best Local Similarity   95.2%;  Pred. No. 6.5e-40;
  Matches   99;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISA 104
              |||||||||||||||||||||||||||||||| | | :|
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATDGGKAA 104


RESULT 11
S31119
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S31119
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31119
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-122 <RAA>
A;Cross-references: UNIPROT:Q8WUK1; EMBL:X62970
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             84.5%;  Score 513.5;  DB 2;  Length 122;
  Best Local Similarity   95.2%;  Pred. No. 7.4e-40;
  Matches  100;  Conservative    1;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAG 105
              |||||||||||||||||||||||||||||||||||:| |  ||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKD-GAVAG 104


RESULT 12
S46392
Ig heavy chain V region (VH-28) - human
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46392
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A;Reference number: S46390; MUID:94254092; PMID:8196048
A;Accession: S46392
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-114 <FIG>
A;Cross-references: EMBL:Z31688; NID:g499306; PIDN:CAA83493.1; PID:g1335145
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             84.3%;  Score 512.5;  DB 2;  Length 114;
  Best Local Similarity   87.8%;  Pred. No. 8.6e-40;
  Matches  101;  Conservative    1;  Mismatches    8;  Indels    5;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              || | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVNLRESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||||      | |:  |  |
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARD-----SGGYWGQGTTV 110


RESULT 13
S29546
Ig heavy chain V region (COS-8 / DP-46) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S29546; S26888
R;Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A;Reference number: S29543
A;Accession: S29546
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z17394; NID:g32843; PIDN:CAA78997.1; PID:g32844
A;Note: designated COS-8
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26888
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TO2>
A;Cross-references: EMBL:Z12346; NID:g32912; PIDN:CAA78216.1; PID:g32913
A;Note: designated DP-46
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             84.2%;  Score 512;  DB 2;  Length 98;
```

```
  Best Local Similarity   100.0%;  Pred. No. 8.1e-40;
  Matches   98;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR 98
              ||||||||||||||||||||||||||||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR 98


RESULT 14
S31111
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31111
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31111
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-119 <RAA>
A;Cross-references: EMBL:X62959
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             84.2%;  Score 512;  DB 2;  Length 119;
  Best Local Similarity   98.0%;  Pred. No. 9.9e-40;
  Matches   98;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||| |||||||||||||||| ||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR 100
              ||||||||||||||||||||||||||||||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR 100


RESULT 15
S31603
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31603
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31603
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-132 <CUI>
A;Cross-references: EMBL:Z14168; NID:g30999; PIDN:CAA78537.1; PID:g31000
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;30-113/Domain: immunoglobulin homology <IMM>

  Query Match             84.1%;  Score 511.5;  DB 2;  Length 132;
  Best Local Similarity   88.3%;  Pred. No. 1.2e-39;
  Matches   98;  Conservative    3;  Mismatches    3;  Indels    7;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db         16 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 75

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYY 111
              ||||||||||||||||||||||||| |||||||||||:|        :||:
Db         76 ADSVKGRFTISRDNSKNTLYLQMNGLRAEDTAVYYCAKDL-------FYYF 119


RESULT 16
S36270
Ig heavy chain V region (clone alpha-TNF-E1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36270
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.,
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36270
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-117 <GRI>
A;Cross-references: EMBL:Z18839; NID:g33118; PIDN:CAA79291.1; PID:g939898
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             83.6%;  Score 508.5;  DB 2;  Length 117;
  Best Local Similarity   85.2%;  Pred. No. 2e-39;
  Matches   98;  Conservative    6;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||| |||||:|||| |||||||||| ||||||||||||||||||||||||||||||||
Db          1 QVQLQESGGGLVQPGGSLRLSCAASGLTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              ||||||||||||||||||||::|||||||||| |:  :   | :||| |||
Db         61 ADSVKGRFTISRDNSKNTLYLQMDNLRAEDTAVYYCVREDYVITSG-FYYYHMDV 114


RESULT 17
PL0098
Ig heavy chain precursor V-III region (FL2-2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Accession: PL0098
R;Nickerson, K.G.; Berman, J.; Glickman, E.; Chess, L.; Alt, F.W.
J. Exp. Med. 169, 1391-1403, 1989
A;Title: Early human IgH gene assembly in Epstein-Barr virus-transformed fetal B cell lir
s.
A;Reference number: PL0098; MUID:89176893; PMID:2538551
A;Accession: PL0098
A;Molecule type: DNA
A;Residues: 1-130 <NIC>
A;Cross-references: UNIPROT:Q8WUK1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;17-120/Product: Ig heavy chain V-III region FL2-2 #status predicted <MAT>
F;32-115/Domain: immunoglobulin homology <IMM>

  Query Match             83.6%;  Score 508;  DB 2;  Length 130;
  Best Local Similarity   89.3%;  Pred. No. 2.5e-39;
  Matches  100;  Conservative    4;  Mismatches    6;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||
Db         18 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQALGKGLEWVAVISYDGSNKYY 77

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYG 112
              |||||||||||||||||||||||||||||||||||:|| :  | :|:  |
Db         78 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDR--NWGFDYWGQG 127


RESULT 18
S31112
Ig heavy chain - human
C;Species: Homo sapiens (man)
```

C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31112
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31112
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-120 <RAA>
A;Cross-references: EMBL:X62961
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 83.4%; Score 507; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.9e-39;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
Db 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA 97
Db 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA 97

RESULT 19
S31117
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31117
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31117
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-122 <RAA>
A;Cross-references: EMBL:X62967
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 83.4%; Score 507; DB 2; Length 122;
Best Local Similarity 98.0%; Pred. No. 2.9e-39;
Matches 97; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
Db 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60

Qy 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARD 99
Db 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARD 99

RESULT 20
PL0116
Ig heavy chain V-III region (AW-Vx) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C;Accession: PL0116; S26892
R;Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin
A;Reference number: PL0116; MUID:88286083; PMID:2840480
A;Accession: PL0116
A;Molecule type: mRNA
A;Residues: 1-98 <BIR>
A;Experimental source: B cells from patient AW with acute lymphoblastic leukemia, ALL
A;Note: the sequence shows the V region (AW-Vx) from a nonproductive DNA rearrangement fr
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26892
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: EMBL:Z12349; NID:g32918; PIDN:CAA78219.1; PID:g32919
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;49-65/Region: complementarity-determining 2

Query Match 83.1%; Score 505; DB 2; Length 98;
Best Local Similarity 98.0%; Pred. No. 3.5e-39;
Matches 96; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
Db 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR 98
Db 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK 98

RESULT 21
S38490
Ig heavy chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S38490
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.
submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a ph
A;Reference number: S38488
A;Accession: S38490
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-113 <MAR>
A;Cross-references: EMBL:Z23030; NID:g414027; PIDN:CAA80565.1; PID:g414028
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 83.1%; Score 505; DB 2; Length 113;
Best Local Similarity 94.2%; Pred. No. 4.1e-39;
Matches 97; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
Db 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGIS 103
Db 61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCASLRGYS 103

RESULT 22
S36259
Ig heavy chain V region (clone alpha-TNF-A1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36259
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.;
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.

```
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36259
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-117 <GRI>
A;Cross-references: EMBL:Z18850; NID:g33123; PIDN:CAA79302.1; PID:g939902
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             83.0%;  Score 504.5;  DB 2;  Length 117;
  Best Local Similarity   84.3%;  Pred. No. 4.7e-39;
  Matches   97;  Conservative    5;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||||||||:|||| |||||||||||||| |||| |||||||||| | ||||||||
Db          1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYGMHWVLQAPGKGLEWVAFIRYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||| |:  :   | |:|| |||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVREDHVITTGRYHYY-MDV 114


RESULT 23
S70442
Ig heavy chain precursor V region (mu) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: S70442
R;Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A;Title: IgM kappa/lambda EBV human B cell clone: an early step of differentiation of fe
A;Reference number: S70442; MUID:93024508; PMID:1383695
A;Accession: S70442
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-140 <CUI>
A;Cross-references: UNIPROT:Q8WUK1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>

  Query Match             82.6%;  Score 502.5;  DB 2;  Length 140;
  Best Local Similarity   86.7%;  Pred. No. 8.6e-39;
  Matches   98;  Conservative    4;  Mismatches    8;  Indels    3;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||| |||||||||||||:| |||||||||||||| | ||||||||
Db         20 QVQLVESGGGVVQPGGSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAFIRYDGSNKYY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYY-YYG 112
              |||||||||||||||||||||||||||||||||||  :  |  |: |:|
Db         80 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDHIV--GATYFDYWG 130


RESULT 24
S31701
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31701
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31701
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137 <CUI>
A;Cross-references: EMBL:Z14177; NID:g31020; PIDN:CAA78546.1; PID:g31021
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

  Query Match             82.1%;  Score 499;  DB 2;  Length 137;
  Best Local Similarity   97.9%;  Pred. No. 1.7e-38;
  Matches   95;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA 97
              |||||||||:|||||||||||||||||||||||||||
Db         80 PDSVKGRFTITRDNSKNTLYLQMNSLRAEDTAVYYCA 116


RESULT 25
I37780
Ig variable region (VDJ) (clone T20-11) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
C;Accession: I37780; S25474
R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable region genes expressed by hu
A;Reference number: A36876; MUID:94119917; PMID:8290556
A;Accession: I37780
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-147 <RES>
A;Cross-references: EMBL:X67943; NID:g33578; PIDN:CAA48130.1; PID:g33579
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;28-111/Domain: immunoglobulin homology <IMM>

  Query Match             81.9%;  Score 498;  DB 2;  Length 147;
  Best Local Similarity   85.2%;  Pred. No. 2.3e-38;
  Matches   98;  Conservative    3;  Mismatches   12;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||||||||:|||| |||||||||||||| | |||||||||||||| |  ||| |||
Db         14 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYY 73

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||:|       | ||||||||
Db         74 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDG--EGWGLYYYYGMDV 126


Search completed: June 16, 2005, 07:44:57
Job time : 26.2377 secs
```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 07:43:15 ; Search time 107.265 Seconds
(without alignments)
411.670 Million cell updates/sec

Title: US-09-920-137D-7
Perfect score: 608
Sequence: 1 QVQLVESGGGVVQPGRSLRL.....CARDRGISAGGNYYYYGMDV 115

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	608	100.0	115	14	US-10-305-347A-7	Sequence 7, Appli
2	608	100.0	115	18	US-10-954-900A-7	Sequence 7, Appli
3	553.5	91.0	123	15	US-10-292-088-117	Sequence 117, App
4	553.5	91.0	138	14	US-10-325-694-144	Sequence 144, App
5	553	91.0	124	15	US-10-371-942-82	Sequence 82, Appl
6	550.5	90.5	125	15	US-10-292-088-107	Sequence 107, App
7	550.5	90.5	138	14	US-10-325-694-150	Sequence 150, App
8	550.5	90.5	252	10	US-09-880-748-1731	Sequence 1731, Ap
9	550.5	90.5	252	15	US-10-293-418-1731	Sequence 1731, Ap
10	550	90.5	126	14	US-10-041-860-17	Sequence 17, Appl
11	550	90.5	126	14	US-10-041-860-209	Sequence 209, App
12	550	90.5	126	14	US-10-041-860-282	Sequence 282, App
13	550	90.5	126	16	US-10-665-383-14	Sequence 14, Appl
14	549.5	90.4	123	15	US-10-292-088-116	Sequence 116, App
15	549	90.3	141	17	US-10-858-855-11	Sequence 11, Appl
16	548	90.1	124	15	US-10-292-088-106	Sequence 106, App
17	547.5	90.0	123	15	US-10-292-088-115	Sequence 115, App
18	546	89.8	126	17	US-10-727-155-128	Sequence 128, App
19	545.5	89.7	125	17	US-10-727-155-206	Sequence 206, App
20	545.5	89.7	125	17	US-10-727-155-218	Sequence 218, App
21	545.5	89.7	125	17	US-10-727-155-222	Sequence 222, App
22	544	89.5	122	9	US-09-144-886-69	Sequence 69, Appl
23	544	89.5	122	16	US-10-632-706-66	Sequence 66, Appl
24	543	89.3	126	14	US-10-041-860-25	Sequence 25, Appl
25	543	89.3	126	14	US-10-041-860-210	Sequence 210, App
26	543	89.3	126	14	US-10-041-860-246	Sequence 246, App
27	543	89.3	126	14	US-10-041-860-306	Sequence 306, App
28	543	89.3	126	16	US-10-665-383-30	Sequence 30, Appl
29	542.5	89.2	451	14	US-10-153-382-17	Sequence 17, Appl
30	542.5	89.2	451	16	US-10-612-497-70	Sequence 70, Appl
31	542.5	89.2	451	16	US-10-776-649-70	Sequence 70, Appl
32	542	89.1	122	9	US-09-144-886-68	Sequence 68, Appl
33	542	89.1	122	16	US-10-632-706-65	Sequence 65, Appl
34	541	89.0	122	17	US-10-727-155-34	Sequence 34, Appl
35	541	89.0	126	14	US-10-041-860-245	Sequence 245, App
36	540.5	88.9	123	15	US-10-269-711-11	Sequence 11, Appl
37	540.5	88.9	123	15	US-10-269-711-23	Sequence 23, Appl
38	540.5	88.9	123	15	US-10-269-711-27	Sequence 27, Appl
39	540.5	88.9	123	15	US-10-269-711-31	Sequence 31, Appl
40	540.5	88.9	123	15	US-10-269-711-35	Sequence 35, Appl
41	540.5	88.9	123	16	US-10-684-109-11	Sequence 11, Appl
42	540.5	88.9	125	15	US-10-292-088-74	Sequence 74, Appl
43	540.5	88.9	470	15	US-10-292-088-78	Sequence 78, Appl
44	540	88.8	134	17	US-10-727-155-254	Sequence 254, App
45	537.5	88.4	123	15	US-10-269-711-43	Sequence 43, Appl
46	537.5	88.4	123	16	US-10-684-109-35	Sequence 35, Appl
47	536.5	88.2	123	15	US-10-269-711-7	Sequence 7, Appli
48	536.5	88.2	123	15	US-10-269-711-15	Sequence 15, Appl
49	536.5	88.2	123	16	US-10-684-109-7	Sequence 7, Appli
50	536.5	88.2	123	16	US-10-684-109-15	Sequence 15, Appl
51	536.5	88.2	125	17	US-10-727-155-104	Sequence 104, App
52	536.5	88.2	125	17	US-10-727-155-174	Sequence 174, App
53	535.5	88.1	125	17	US-10-727-155-6	Sequence 6, Appli
54	535.5	88.1	127	17	US-10-706-689-36	Sequence 36, Appl
55	534	87.8	124	17	US-10-727-155-42	Sequence 42, Appl
56	534	87.8	249	10	US-09-880-748-512	Sequence 512, App
57	534	87.8	249	15	US-10-293-418-512	Sequence 512, App
58	533	87.7	126	10	US-09-848-798-26	Sequence 26, Appl
59	532.5	87.6	123	17	US-10-727-155-124	Sequence 124, App
60	532.5	87.6	127	15	US-10-309-762-150	Sequence 150, App
61	532.5	87.6	144	15	US-10-395-894-31	Sequence 31, Appl
62	532.5	87.6	144	16	US-10-695-667-31	Sequence 31, Appl
63	531	87.3	126	15	US-10-309-762-133	Sequence 133, App
64	530.5	87.3	127	17	US-10-706-689-22	Sequence 22, Appl
65	529.5	87.1	123	17	US-10-727-155-132	Sequence 132, App
66	528.5	86.9	252	10	US-09-880-748-1394	Sequence 1394, Ap
67	528.5	86.9	252	15	US-10-293-418-1394	Sequence 1394, Ap
68	527	86.7	126	10	US-09-848-798-153	Sequence 153, App
69	527	86.7	254	10	US-09-880-748-981	Sequence 981, App
70	527	86.7	254	15	US-10-293-418-981	Sequence 981, App
71	526.5	86.6	119	17	US-10-706-689-18	Sequence 18, Appl
72	526.5	86.6	125	17	US-10-727-155-58	Sequence 58, Appl
73	526.5	86.6	125	17	US-10-727-155-62	Sequence 62, Appl
74	526	86.5	120	14	US-10-330-613-29	Sequence 29, Appl
75	526	86.5	120	14	US-10-330-530-29	Sequence 29, Appl
76	526	86.5	120	16	US-10-660-357-29	Sequence 29, Appl
77	526	86.5	247	10	US-09-880-748-1330	Sequence 1330, Ap
78	526	86.5	247	15	US-10-293-418-1330	Sequence 1330, Ap
79	526	86.5	249	10	US-09-880-748-1724	Sequence 1724, Ap
80	526	86.5	249	10	US-09-880-748-1725	Sequence 1725, Ap
81	526	86.5	249	15	US-10-293-418-1724	Sequence 1724, Ap
82	526	86.5	249	15	US-10-293-418-1725	Sequence 1725, Ap
83	526	86.5	256	10	US-09-880-748-839	Sequence 839, App
84	526	86.5	256	15	US-10-293-418-839	Sequence 839, App

85	525.5	86.4	121	15	US-10-309-762-132	Sequence 132, App
86	525	86.3	126	10	US-09-848-798-25	Sequence 25, Appl
87	524.5	86.3	125	15	US-10-292-088-58	Sequence 58, Appl
88	524.5	86.3	470	15	US-10-292-088-62	Sequence 62, Appl
89	523	86.0	143	15	US-10-395-894-19	Sequence 19, Appl
90	523	86.0	143	16	US-10-695-667-19	Sequence 19, Appl
91	523	86.0	249	10	US-09-880-748-397	Sequence 397, App
92	523	86.0	249	10	US-09-880-748-1102	Sequence 1102, Ap
93	523	86.0	249	10	US-09-880-748-1115	Sequence 1115, Ap
94	523	86.0	249	15	US-10-293-418-397	Sequence 397, App
95	523	86.0	249	15	US-10-293-418-1102	Sequence 1102, Ap
96	523	86.0	249	15	US-10-293-418-1115	Sequence 1115, Ap
97	522.5	85.9	142	15	US-10-395-894-15	Sequence 15, Appl
98	522.5	85.9	142	16	US-10-695-667-15	Sequence 15, Appl
99	522	85.9	124	17	US-10-727-155-38	Sequence 38, Appl
100	521	85.7	128	17	US-10-727-155-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1
US-10-305-347A-7
; Sequence 7, Application US/10305347A
; Publication No. US20030143603A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Bernie Scallon
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5005
; CURRENT APPLICATION NUMBER: US/10/305,347A
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 7
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-305-347A-7

Query Match 100.0%; Score 608; DB 14; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.1e-48;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
```

RESULT 2
US-10-954-900A-7
; Sequence 7, Application US/10954900A
; Publication No. US20050123541A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: David Shealy
; APPLICANT: David Knight
; APPLICANT: Bernie Scallon
; APPLICANT: George Heavner
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0250 DIV-2
; CURRENT APPLICATION NUMBER: US/10/954,900A
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 09/920,262
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,360
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,826
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 7
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-954-900A-7

Query Match 100.0%; Score 608; DB 18; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.1e-48;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
```

RESULT 3
US-10-292-088-117
; Sequence 117, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 117
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-117

Query Match 91.0%; Score 553.5; DB 15; Length 123;
Best Local Similarity 93.9%; Pred. No. 2.3e-43;
Matches 108; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

```
Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||||||| |       ||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDYG---DYYYYYGMDV 112
```

RESULT 4
US-10-325-694-144
; Sequence 144, Application US/10325694
; Publication No. US20030148463A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RAUM, TOBIAS
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF
; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/10/325,694
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/403,107
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152

```
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 144
;   LENGTH: 138
;   TYPE: PRT
;   ORGANISM: HUMAN
US-10-325-694-144

  Query Match             91.0%;  Score 553.5;  DB 14;  Length 138;
  Best Local Similarity   91.4%;  Pred. No. 2.6e-43;
  Matches  106;  Conservative    3;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGN-YYYYGMDV 115
              |||||||||||||||||||||||||||||:| |  :|   ||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDMGWGSGWRPYYYYGMDV 116


RESULT 5
US-10-371-942-82
; Sequence 82, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
;  APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
;  APPLICANT:  Reiter, Yoram
;  TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
;  FILE REFERENCE: 10280-034001
;  CURRENT APPLICATION NUMBER: US/10/371,942
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/358,994
;  PRIOR FILING DATE: 2002-02-20
;  NUMBER OF SEQ ID NOS: 121
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 82
;   LENGTH: 124
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-371-942-82

  Query Match             91.0%;  Score 553;  DB 15;  Length 124;
  Best Local Similarity   92.2%;  Pred. No. 2.6e-43;
  Matches  106;  Conservative    2;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||:|||||||||||||||||||||||| |||||||||||||||||||||||||||
Db          1 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||     | :||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARD--FDYGDSYYYYGMDV 113


RESULT 6
US-10-292-088-107
; Sequence 107, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
;  APPLICANT: BEDIAN, VAHE
;  APPLICANT:  GLADUE, RONALD P.
;  APPLICANT:  CORVALAN, JOSE
;  APPLICANT:  JIA, XIAO-CHI
;  APPLICANT:  FENG, XIAO
;  TITLE OF INVENTION: ANTIBODIES TO CD40
;  FILE REFERENCE: ABX-PF/3 US
;  CURRENT APPLICATION NUMBER: US/10/292,088
;  CURRENT FILING DATE:  2003-03-14
;  PRIOR APPLICATION NUMBER: 60/348,980
;  PRIOR FILING DATE: 2001-11-09
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
;   LENGTH: 125
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-292-088-107

  Query Match             90.5%;  Score 550.5;  DB 15;  Length 125;
  Best Local Similarity   93.0%;  Pred. No. 4.5e-43;
  Matches  107;  Conservative    0;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||  | |    ||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR-MGSSGSDYYYYYGMDV 114


RESULT 7
US-10-325-694-150
; Sequence 150, Application US/10325694
; Publication No. US20030148463A1
; GENERAL INFORMATION:
;  APPLICANT: KUFER, PETER
;  APPLICANT:  RAUM, TOBIAS
;  TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
;  TITLE OF INVENTION:  RECEPTORS AND USES THEREOF
;  FILE REFERENCE: 38164000
;  CURRENT APPLICATION NUMBER: US/10/325,694
;  CURRENT FILING DATE:  2002-12-19
;  PRIOR APPLICATION NUMBER: US/09/403,107
;  PRIOR FILING DATE: 1999-10-14
;  NUMBER OF SEQ ID NOS: 152
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 150
;   LENGTH: 138
;   TYPE: PRT
;   ORGANISM: HUMAN
US-10-325-694-150

  Query Match             90.5%;  Score 550.5;  DB 14;  Length 138;
  Best Local Similarity   90.5%;  Pred. No. 5e-43;
  Matches  105;  Conservative    4;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||:|||||||||||||||||||||||| |||||||||||||||||||||||||||
Db          1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGN-YYYYGMDV 115
              |||||||||||||||||||||||||||||||||||:| |  :|   ||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDMGWGSGWRPYYYYGMDV 116


RESULT 8
US-09-880-748-1731
; Sequence 1731, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
```

```
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1731
;   LENGTH: 252
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-1731

  Query Match            90.5%;  Score 550.5;  DB 10;  Length 252;
  Best Local Similarity   91.6%;  Pred. No. 9.4e-43;
  Matches  109;  Conservative    0;  Mismatches    5;  Indels    5;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR----GISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||||||     |   | ||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRLEYYDILT-GYYYYYGMDV 118


RESULT 9
US-10-293-418-1731
; Sequence 1731, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P2
;  CURRENT APPLICATION NUMBER: US/10/293,418
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-16
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1731
;   LENGTH: 252
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-293-418-1731

  Query Match            90.5%;  Score 550.5;  DB 15;  Length 252;
  Best Local Similarity   91.6%;  Pred. No. 9.4e-43;
  Matches  109;  Conservative    0;  Mismatches    5;  Indels    5;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR----GISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||||||     |   | ||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRLEYYDILT-GYYYYYGMDV 118


RESULT 10
US-10-041-860-17
; Sequence 17, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
;  APPLICANT: Corvalan, Jose R.F.
;  APPLICANT:  Jia, Xiao-Chi
;  APPLICANT:  Feng, Xiao
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Chen, Francine
;  APPLICANT:  Gazit, Gadi
;  APPLICANT:  Weber, Richard
;  APPLICANT:  Bezabeh, Binyam
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: ABGENIX.051A
;  CURRENT APPLICATION NUMBER: US/10/041,860
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 377
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 126
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-041-860-17

  Query Match            90.5%;  Score 550;  DB 14;  Length 126;
  Best Local Similarity   91.3%;  Pred. No. 5e-43;
  Matches  105;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||||:|||||||||||||| |||||||||||||||||||| ||||||||
Db          1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||:|    | || |||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGYRYAGYYYDYGMDV 115


RESULT 11
US-10-041-860-209
; Sequence 209, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
;  APPLICANT: Corvalan, Jose R.F.
;  APPLICANT:  Jia, Xiao-Chi
;  APPLICANT:  Feng, Xiao
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Chen, Francine
;  APPLICANT:  Gazit, Gadi
;  APPLICANT:  Weber, Richard
;  APPLICANT:  Bezabeh, Binyam
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: ABGENIX.051A
;  CURRENT APPLICATION NUMBER: US/10/041,860
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 377
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 209
;   LENGTH: 126
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-041-860-209

  Query Match            90.5%;  Score 550;  DB 14;  Length 126;
  Best Local Similarity   91.3%;  Pred. No. 5e-43;
  Matches  105;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||||:|||||||||||||| |||||||||||||||||||| ||||||||
Db          1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||:|    | || |||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGYRYAGYYYDYGMDV 115


RESULT 12
```

```
US-10-041-860-282
; Sequence 282, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
;  APPLICANT: Corvalan, Jose R.F.
;  APPLICANT:  Jia, Xiao-Chi
;  APPLICANT:  Feng, Xiao
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Chen, Francine
;  APPLICANT:  Gazit, Gadi
;  APPLICANT:  Weber, Richard
;  APPLICANT:  Bezabeh, Binyam
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: ABGENIX.051A
;  CURRENT APPLICATION NUMBER: US/10/041,860
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 377
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 282
;   LENGTH: 126
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-041-860-282

  Query Match             90.5%;  Score 550;  DB 14;  Length 126;
  Best Local Similarity   91.3%;  Pred. No. 5e-43;
  Matches  105;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||:|||||||||||||||| ||||||||||||||||||| ||||||||
Db          1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||:|    | || |||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGYRYAGYYYDYGMDV 115


RESULT 13
US-10-665-383-14
; Sequence 14, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
;  APPLICANT: Floege, Juergen
;  APPLICANT:  Gazit, Gadi
;  APPLICANT:  Keyt, Bruce
;  APPLICANT:  LaRochelle, William
;  APPLICANT:  Lichenstein, Henri
;  TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
;  TITLE OF INVENTION:  USING ANTI-PDGF-DD ANTIBODIES
;  FILE REFERENCE: ABGENIX.052A
;  CURRENT APPLICATION NUMBER: US/10/665,383
;  CURRENT FILING DATE:  2003-09-16
;  PRIOR APPLICATION NUMBER: 60/411,137
;  PRIOR FILING DATE: 2002-09-16
;  NUMBER OF SEQ ID NOS: 97
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 126
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-665-383-14

  Query Match             90.5%;  Score 550;  DB 16;  Length 126;
  Best Local Similarity   91.3%;  Pred. No. 5e-43;
  Matches  105;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||:|||||||||||||||| ||||||||||||||||||| ||||||||
Db          1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||:|    | || |||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGYRYAGYYYDYGMDV 115


RESULT 14
US-10-292-088-116
; Sequence 116, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
;  APPLICANT: BEDIAN, VAHE
;  APPLICANT:  GLADUE, RONALD P.
;  APPLICANT:  CORVALAN, JOSE
;  APPLICANT:  JIA, XIAO-CHI
;  APPLICANT:  FENG, XIAO
;  TITLE OF INVENTION: ANTIBODIES TO CD40
;  FILE REFERENCE: ABX-PF/3 US
;  CURRENT APPLICATION NUMBER: US/10/292,088
;  CURRENT FILING DATE:  2003-03-14
;  PRIOR APPLICATION NUMBER: 60/348,980
;  PRIOR FILING DATE: 2001-11-09
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 116
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-292-088-116

  Query Match             90.4%;  Score 549.5;  DB 15;  Length 123;
  Best Local Similarity   93.0%;  Pred. No. 5.5e-43;
  Matches  107;  Conservative    0;  Mismatches    5;  Indels    3;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              ||||||||||||||||||||||||||||||||||||| |      ||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDYG---DYYYYYGMDV 112


RESULT 15
US-10-858-855-11
; Sequence 11, Application US/10858855
; Publication No. US20050118651A1
; GENERAL INFORMATION:
;  APPLICANT: BASI, Guriq
;  TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA
;  TITLE OF INVENTION:  AMYLOID PEPTIDE
;  FILE REFERENCE: ELN-028
;  CURRENT APPLICATION NUMBER: US/10/858,855
;  CURRENT FILING DATE:  2004-06-01
;  PRIOR APPLICATION NUMBER: 60/474654
;  PRIOR FILING DATE: 2003-05-30
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 141
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(19)
US-10-858-855-11

  Query Match             90.3%;  Score 549;  DB 17;  Length 141;
  Best Local Similarity   93.0%;  Pred. No. 7e-43;
  Matches  107;  Conservative    2;  Mismatches    2;  Indels    4;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
```

```
                ||||||||||||||||||||||||||||||||||||||||  |:    :||||||
Db         80 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRHSSS----WYYGMDV 130


RESULT 16
US-10-292-088-106
; Sequence 106, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
;  APPLICANT: BEDIAN, VAHE
;  APPLICANT:  GLADUE, RONALD P.
;  APPLICANT:  CORVALAN, JOSE
;  APPLICANT:  JIA, XIAO-CHI
;  APPLICANT:  FENG, XIAO
;  TITLE OF INVENTION: ANTIBODIES TO CD40
;  FILE REFERENCE: ABX-PF/3 US
;  CURRENT APPLICATION NUMBER: US/10/292,088
;  CURRENT FILING DATE:  2003-03-14
;  PRIOR APPLICATION NUMBER: 60/348,980
;  PRIOR FILING DATE: 2001-11-09
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
;   LENGTH: 124
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-292-088-106

  Query Match             90.1%;  Score 548;  DB 15;  Length 124;
  Best Local Similarity   93.0%;  Pred. No. 7.6e-43;
  Matches  107;  Conservative    0;  Mismatches    6;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||  ||    | ||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA--RGHQLLGYYYYYGMDV 113


RESULT 17
US-10-292-088-115
; Sequence 115, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
;  APPLICANT: BEDIAN, VAHE
;  APPLICANT:  GLADUE, RONALD P.
;  APPLICANT:  CORVALAN, JOSE
;  APPLICANT:  JIA, XIAO-CHI
;  APPLICANT:  FENG, XIAO
;  TITLE OF INVENTION: ANTIBODIES TO CD40
;  FILE REFERENCE: ABX-PF/3 US
;  CURRENT APPLICATION NUMBER: US/10/292,088
;  CURRENT FILING DATE:  2003-03-14
;  PRIOR APPLICATION NUMBER: 60/348,980
;  PRIOR FILING DATE: 2001-11-09
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 115
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-292-088-115

  Query Match             90.0%;  Score 547.5;  DB 15;  Length 123;
  Best Local Similarity   92.2%;  Pred. No. 8.4e-43;
  Matches  106;  Conservative    1;  Mismatches    5;  Indels    3;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||||    : |  ||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARG---TTGTYYYYYGMDV 112


RESULT 18
US-10-727-155-128
; Sequence 128, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
;  APPLICANT: John S. Babcook
;  APPLICANT:  Jaspal S. Kang
;  APPLICANT:  Orit Foord
;  APPLICANT:  Larry Green
;  APPLICANT:  Xiao Feng
;  APPLICANT:  Scott Klakamp
;  APPLICANT:  Mary Haak-Frendscho
;  APPLICANT:  Palaniswami Rathanaswami
;  APPLICANT:  Craig Pigott
;  APPLICANT:  Meina Liang
;  APPLICANT:  Rozanne Lee
;  APPLICANT:  Kathy Manchulencho
;  APPLICANT:  Raffaella Faggioni
;  APPLICANT:  Giorgio Senaldi
;  APPLICANT:  Qiaojuan Jane Su
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
;  TITLE OF INVENTION:  FACTOR AND USES THEREOF
;  FILE REFERENCE: ABGENIX.073A
;  CURRENT APPLICATION NUMBER: US/10/727,155
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: 60/430729
;  PRIOR FILING DATE: 2002-12-02
;  NUMBER OF SEQ ID NOS: 320
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 128
;   LENGTH: 126
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-727-155-128

  Query Match             89.8%;  Score 546;  DB 17;  Length 126;
  Best Local Similarity   91.3%;  Pred. No. 1.2e-42;
  Matches  105;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||:| |||||||||||||||| ||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||:    ||  ||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREGIAVAGPPYYYYGMDV 115


RESULT 19
US-10-727-155-206
; Sequence 206, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
;  APPLICANT: John S. Babcook
;  APPLICANT:  Jaspal S. Kang
;  APPLICANT:  Orit Foord
;  APPLICANT:  Larry Green
;  APPLICANT:  Xiao Feng
;  APPLICANT:  Scott Klakamp
;  APPLICANT:  Mary Haak-Frendscho
;  APPLICANT:  Palaniswami Rathanaswami
;  APPLICANT:  Craig Pigott
;  APPLICANT:  Meina Liang
;  APPLICANT:  Rozanne Lee
;  APPLICANT:  Kathy Manchulencho
;  APPLICANT:  Raffaella Faggioni
;  APPLICANT:  Giorgio Senaldi
;  APPLICANT:  Qiaojuan Jane Su
```

```
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
;  TITLE OF INVENTION:  FACTOR AND USES THEREOF
;  FILE REFERENCE: ABGENIX.073A
;  CURRENT APPLICATION NUMBER: US/10/727,155
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: 60/430729
;  PRIOR FILING DATE: 2002-12-02
;  NUMBER OF SEQ ID NOS: 320
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 206
;   LENGTH: 125
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-727-155-206

  Query Match             89.7%;  Score 545.5;  DB 17;  Length 125;
  Best Local Similarity   91.3%;  Pred. No. 1.3e-42;
  Matches  105;  Conservative    3;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||||||||||||||||||| |||||||||||||||| ||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||:  ::  | ||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARETTVTKEG-YYYYGMDV 114


RESULT 20
US-10-727-155-218
; Sequence 218, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
;  APPLICANT: John S. Babcook
;  APPLICANT:  Jaspal S. Kang
;  APPLICANT:  Orit Foord
;  APPLICANT:  Larry Green
;  APPLICANT:  Xiao Feng
;  APPLICANT:  Scott Klakamp
;  APPLICANT:  Mary Haak-Frendscho
;  APPLICANT:  Palaniswami Rathanaswami
;  APPLICANT:  Craig Pigott
;  APPLICANT:  Meina Liang
;  APPLICANT:  Rozanne Lee
;  APPLICANT:  Kathy Manchulencho
;  APPLICANT:  Raffaella Faggioni
;  APPLICANT:  Giorgio Senaldi
;  APPLICANT:  Qiaojuan Jane Su
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
;  TITLE OF INVENTION:  FACTOR AND USES THEREOF
;  FILE REFERENCE: ABGENIX.073A
;  CURRENT APPLICATION NUMBER: US/10/727,155
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: 60/430729
;  PRIOR FILING DATE: 2002-12-02
;  NUMBER OF SEQ ID NOS: 320
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 218
;   LENGTH: 125
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-727-155-218

  Query Match             89.7%;  Score 545.5;  DB 17;  Length 125;
  Best Local Similarity   91.3%;  Pred. No. 1.3e-42;
  Matches  105;  Conservative    3;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||||||||||||||||||| |||||||||||||||| ||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||:  ::  | ||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARETTVTKEG-YYYYGMDV 114


RESULT 21
US-10-727-155-222
; Sequence 222, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
;  APPLICANT: John S. Babcook
;  APPLICANT:  Jaspal S. Kang
;  APPLICANT:  Orit Foord
;  APPLICANT:  Larry Green
;  APPLICANT:  Xiao Feng
;  APPLICANT:  Scott Klakamp
;  APPLICANT:  Mary Haak-Frendscho
;  APPLICANT:  Palaniswami Rathanaswami
;  APPLICANT:  Craig Pigott
;  APPLICANT:  Meina Liang
;  APPLICANT:  Rozanne Lee
;  APPLICANT:  Kathy Manchulencho
;  APPLICANT:  Raffaella Faggioni
;  APPLICANT:  Giorgio Senaldi
;  APPLICANT:  Qiaojuan Jane Su
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
;  TITLE OF INVENTION:  FACTOR AND USES THEREOF
;  FILE REFERENCE: ABGENIX.073A
;  CURRENT APPLICATION NUMBER: US/10/727,155
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: 60/430729
;  PRIOR FILING DATE: 2002-12-02
;  NUMBER OF SEQ ID NOS: 320
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 222
;   LENGTH: 125
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-727-155-222

  Query Match             89.7%;  Score 545.5;  DB 17;  Length 125;
  Best Local Similarity   90.4%;  Pred. No. 1.3e-42;
  Matches  104;  Conservative    5;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||||||||||||||||||| |||||||||||||||:|||||| |||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAIISYDGSIKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||:  :: || ||:|||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARENAVTYGG-YYHYGMDV 114


RESULT 22
US-09-144-886-69
; Sequence 69, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
;  APPLICANT: Marks, James D
;  APPLICANT: Amersdorfer, Peter
;  TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
;  TITLE OF INVENTION: Botulinum Neurotoxins
;  FILE REFERENCE: 2500.117USO
;  CURRENT APPLICATION NUMBER: US/09/144,886
;  CURRENT FILING DATE: 1998-08-31
;  NUMBER OF SEQ ID NOS: 98
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
;   LENGTH: 122
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone
;   OTHER INFORMATION: 1C6 region VH epitope 3
US-09-144-886-69
```

```
  Query Match             89.5%;  Score 544;  DB 9;  Length 122;
  Best Local Similarity   92.2%;  Pred. No. 1.7e-42;
  Matches  106;  Conservative    3;  Mismatches    2;  Indels    4;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |:||::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QIQLLQSGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              ||||||||||||||||||||||||||||||||||||   | |  ||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARD--WSEG--YYYYGMDV 111


RESULT 23
US-10-632-706-66
; Sequence 66, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
;  APPLICANT: MARKS, JAMES D.
;  APPLICANT:  AMERSDORFER, PETER
;  TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
;  TITLE OF INVENTION:  NEUROTOXINS
;  FILE REFERENCE: 407T-895120US
;  CURRENT APPLICATION NUMBER: US/10/632,706
;  CURRENT FILING DATE:  2003-08-01
;  PRIOR APPLICATION NUMBER: US 60/400,721
;  PRIOR FILING DATE: 2002-08-01
;  PRIOR APPLICATION NUMBER: US 09/144,806
;  PRIOR FILING DATE: 1998-08-31
;  NUMBER OF SEQ ID NOS: 278
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
;   LENGTH: 122
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: single chain antibody
US-10-632-706-66

  Query Match             89.5%;  Score 544;  DB 16;  Length 122;
  Best Local Similarity   92.2%;  Pred. No. 1.7e-42;
  Matches  106;  Conservative    3;  Mismatches    2;  Indels    4;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |:||::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QIQLLQSGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              ||||||||||||||||||||||||||||||||||||   | |  ||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARD--WSEG--YYYYGMDV 111


RESULT 24
US-10-041-860-25
; Sequence 25, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
;  APPLICANT: Corvalan, Jose R.F.
;  APPLICANT:  Jia, Xiao-Chi
;  APPLICANT:  Feng, Xiao
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Chen, Francine
;  APPLICANT:  Gazit, Gadi
;  APPLICANT:  Weber, Richard
;  APPLICANT:  Bezabeh, Binyam
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: ABGENIX.051A
;  CURRENT APPLICATION NUMBER: US/10/041,860
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 377
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 126
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-041-860-25

  Query Match             89.3%;  Score 543;  DB 14;  Length 126;
  Best Local Similarity   91.3%;  Pred. No. 2.2e-42;
  Matches  105;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||||||||||||||||:|||| |||||||||||||||| | ||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQAPGKGLEWVADIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              ||||||||||||||||||||||||||||||||||||:| | |  || |||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGYSYGYVYYYDYGMDV 115


RESULT 25
US-10-041-860-210
; Sequence 210, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
;  APPLICANT: Corvalan, Jose R.F.
;  APPLICANT:  Jia, Xiao-Chi
;  APPLICANT:  Feng, Xiao
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Chen, Francine
;  APPLICANT:  Gazit, Gadi
;  APPLICANT:  Weber, Richard
;  APPLICANT:  Bezabeh, Binyam
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: ABGENIX.051A
;  CURRENT APPLICATION NUMBER: US/10/041,860
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 377
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 210
;   LENGTH: 126
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-041-860-210

  Query Match             89.3%;  Score 543;  DB 14;  Length 126;
  Best Local Similarity   91.3%;  Pred. No. 2.2e-42;
  Matches  105;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||||||||||||||||:|||| |||||||||||||||| | ||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYGMHWVRQAPGKGLEWVADIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              ||||||||||||||||||||||||||||||||||||:| | |  || |||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGYSYGYVYYYDYGMDV 115


Search completed: June 16, 2005, 08:01:33
Job time : 109.265 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 07:35:01 ; Search time 31.4574 Seconds
(without alignments)
272.897 Million cell updates/sec

Title: US-09-920-137D-7
Perfect score: 608
Sequence: 1 QVQLVESGGGVVQPGRSLRL.....CARDRGISAGGNYYYYGMDV 115

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	542.5	89.2	451	4	US-09-472-087-70	Sequence 70, Appl
2	533	87.7	126	3	US-09-240-274-26	Sequence 26, Appl
3	527	86.7	126	3	US-09-240-274-153	Sequence 153, App
4	525	86.3	120	1	US-07-942-245-35	Sequence 35, Appl
5	525	86.3	126	3	US-09-240-274-25	Sequence 25, Appl
6	524	86.2	123	3	US-08-983-607-38	Sequence 38, Appl
7	519	85.4	115	4	US-09-726-219A-167	Sequence 167, App
8	518	85.2	116	1	US-08-211-202-141	Sequence 141, App
9	515.5	84.8	128	1	US-08-478-039-96	Sequence 96, Appl
10	515.5	84.8	128	1	US-08-476-349A-96	Sequence 96, Appl
11	514.5	84.6	123	4	US-09-424-840B-6	Sequence 6, Appli
12	513	84.4	119	1	US-08-331-398A-46	Sequence 46, Appl
13	513	84.4	119	2	US-08-331-397B-46	Sequence 46, Appl
14	513	84.4	119	2	US-08-759-804A-46	Sequence 46, Appl
15	513	84.4	119	3	US-09-227-693-46	Sequence 46, Appl
16	512	84.2	98	1	US-08-211-202-118	Sequence 118, App
17	511.5	84.1	248	4	US-09-315-926A-80	Sequence 80, Appl
18	511	84.0	310	3	US-09-079-029-11	Sequence 11, Appl
19	510	83.9	117	3	US-09-025-769B-24	Sequence 24, Appl
20	510	83.9	117	4	US-09-490-070A-24	Sequence 24, Appl
21	510	83.9	117	4	US-09-490-153-24	Sequence 24, Appl
22	510	83.9	117	4	US-09-490-324-24	Sequence 24, Appl
23	508	83.6	117	3	US-08-545-809A-115	Sequence 115, App
24	502	82.6	124	4	US-09-424-840B-16	Sequence 16, Appl
25	501	82.4	120	1	US-08-211-202-135	Sequence 135, App
26	501	82.4	225	4	US-09-456-090A-60	Sequence 60, Appl
27	501	82.4	225	4	US-09-456-090A-92	Sequence 92, Appl
28	501	82.4	225	4	US-09-453-234-60	Sequence 60, Appl
29	501	82.4	225	4	US-09-453-234-92	Sequence 92, Appl
30	499.5	82.2	167	4	US-09-472-087-80	Sequence 80, Appl
31	498	81.9	125	3	US-09-240-274-8	Sequence 8, Appli
32	498	81.9	125	3	US-09-240-274-20	Sequence 20, Appl
33	498	81.9	125	3	US-09-240-274-21	Sequence 21, Appl
34	498	81.9	125	3	US-09-240-274-22	Sequence 22, Appl
35	498	81.9	126	3	US-09-240-274-152	Sequence 152, App
36	497.5	81.8	287	3	US-08-862-124-17	Sequence 17, Appl
37	497.5	81.8	304	3	US-08-862-124-14	Sequence 14, Appl
38	497	81.7	123	4	US-09-560-198A-2	Sequence 2, Appli
39	497	81.7	128	3	US-09-240-274-1	Sequence 1, Appli
40	495.5	81.5	125	3	US-09-240-274-140	Sequence 140, App
41	495	81.4	125	2	US-08-428-197-5	Sequence 5, Appli
42	495	81.4	125	2	US-08-428-197-6	Sequence 6, Appli
43	495	81.4	125	5	PCT-US93-10555-5	Sequence 5, Appli
44	495	81.4	125	5	PCT-US93-10555-6	Sequence 6, Appli
45	495	81.4	225	4	US-09-456-090A-106	Sequence 106, App
46	495	81.4	225	4	US-09-453-234-106	Sequence 106, App
47	494.5	81.3	141	1	US-08-259-372A-2	Sequence 2, Appli
48	494.5	81.3	141	1	US-08-468-671-2	Sequence 2, Appli
49	493	81.1	123	4	US-09-560-198A-4	Sequence 4, Appli
50	493	81.1	225	4	US-09-456-090A-56	Sequence 56, Appl
51	493	81.1	225	4	US-09-456-090A-108	Sequence 108, App
52	493	81.1	225	4	US-09-453-234-56	Sequence 56, Appl
53	493	81.1	225	4	US-09-453-234-108	Sequence 108, App
54	492	80.9	123	4	US-09-560-198A-10	Sequence 10, Appl
55	491	80.8	128	3	US-09-240-274-142	Sequence 142, App
56	491	80.8	128	4	US-09-840-459-77	Sequence 77, Appl
57	491	80.8	128	4	US-09-840-459-79	Sequence 79, Appl
58	491	80.8	128	4	US-09-497-625A-77	Sequence 77, Appl
59	491	80.8	128	4	US-09-497-625A-79	Sequence 79, Appl
60	490.5	80.7	463	4	US-09-472-087-4	Sequence 4, Appli
61	490.5	80.7	463	4	US-09-472-087-68	Sequence 68, Appl
62	490	80.6	125	3	US-09-240-274-23	Sequence 23, Appl
63	489	80.4	126	3	US-09-240-274-146	Sequence 146, App
64	488	80.3	123	1	US-08-478-039-94	Sequence 94, Appl
65	488	80.3	123	1	US-08-476-349A-94	Sequence 94, Appl
66	488	80.3	123	4	US-09-424-840B-22	Sequence 22, Appl
67	488	80.3	126	3	US-09-240-274-17	Sequence 17, Appl
68	488	80.3	225	4	US-09-456-090A-102	Sequence 102, App
69	488	80.3	225	4	US-09-453-234-102	Sequence 102, App
70	488	80.3	464	4	US-09-472-087-2	Sequence 2, Appli
71	488	80.3	464	4	US-09-472-087-66	Sequence 66, Appl
72	487.5	80.2	127	3	US-09-240-274-139	Sequence 139, App
73	487	80.1	117	3	US-08-545-809A-117	Sequence 117, App
74	487	80.1	225	4	US-09-456-090A-94	Sequence 94, Appl
75	487	80.1	225	4	US-09-453-234-94	Sequence 94, Appl
76	486.5	80.0	263	3	US-09-069-821-3	Sequence 3, Appli
77	486.5	80.0	263	4	US-09-956-086-3	Sequence 3, Appli
78	486.5	80.0	263	4	US-09-956-087-3	Sequence 3, Appli
79	486.5	80.0	283	3	US-09-420-592A-6	Sequence 6, Appli
80	486.5	80.0	283	4	US-09-985-442-6	Sequence 6, Appli
81	486.5	80.0	283	4	US-09-983-580-6	Sequence 6, Appli
82	486.5	80.0	463	4	US-09-472-087-1	Sequence 1, Appli
83	486.5	80.0	463	4	US-09-472-087-63	Sequence 63, Appl
84	486.5	80.0	463	4	US-09-472-087-64	Sequence 64, Appl
85	486	79.9	225	4	US-09-456-090A-100	Sequence 100, App
86	486	79.9	225	4	US-09-456-090A-110	Sequence 110, App
87	486	79.9	225	4	US-09-453-234-100	Sequence 100, App
88	486	79.9	225	4	US-09-453-234-110	Sequence 110, App
89	485.5	79.9	122	2	US-07-934-373C-21	Sequence 21, Appl
90	485.5	79.9	122	3	US-08-437-642B-21	Sequence 21, Appl
91	485.5	79.9	122	4	US-08-146-206C-21	Sequence 21, Appl
92	485.5	79.9	122	4	US-09-705-686-21	Sequence 21, Appl
93	485.5	79.9	122	4	US-09-705-392A-21	Sequence 21, Appl
94	485.5	79.9	122	4	US-09-705-398-21	Sequence 21, Appl
95	485.5	79.9	122	5	PCT-US93-07832-21	Sequence 21, Appl
96	485.5	79.9	167	4	US-09-472-087-9	Sequence 9, Appli
97	485	79.8	126	3	US-09-240-274-13	Sequence 13, Appl
98	484	79.6	125	3	US-09-240-274-24	Sequence 24, Appl
99	483	79.4	125	3	US-09-240-274-9	Sequence 9, Appli
100	483	79.4	225	4	US-09-456-090A-68	Sequence 68, Appl

ALIGNMENTS

```
RESULT 1
US-09-472-087-70
; Sequence 70, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-70

  Query Match             89.2%;  Score 542.5;  DB 4;  Length 451;
  Best Local Similarity   92.2%;  Pred. No. 4.4e-48;
  Matches  107;  Conservative    1;  Mismatches    5;  Indels    3;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||||||||||||||||||| |||||||||||||||| ||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARD-RGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||| || :    ||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDPRGATL--YYYYYGMDV 114


RESULT 2
US-09-240-274-26
; Sequence 26, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
;   LENGTH: 126
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain D31
US-09-240-274-26

  Query Match             87.7%;  Score 533;  DB 3;  Length 126;
  Best Local Similarity   86.1%;  Pred. No. 9.2e-48;
  Matches   99;  Conservative    9;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||:|||||||||||||||||||||||||| |||||||||||||||: ||||||:|
Db          1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVVYYDGSNKHY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              :|||||||||||||||||||:|||||||||||||||:|   :| : |||||||
Db         61 SDSVKGRFTISRDNSKNTLYLQMDSLRAEDTAVYYCARERNFRSGYSRYYYGMDV 115


RESULT 3
US-09-240-274-153
; Sequence 153, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 153
;   LENGTH: 126
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH56
US-09-240-274-153

  Query Match             86.7%;  Score 527;  DB 3;  Length 126;
  Best Local Similarity   85.2%;  Pred. No. 3.8e-47;
  Matches   98;  Conservative    9;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||:|||||||||||||||||||||||||| |||||||||||||||: ||||||:|
Db          1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVVYYDGSNKHY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              :||||||||| ||||||||||:|||||||||||||:|   :| : |||||||
Db         61 SDSVKGRFTIFRDNSKNTLYLQMDSLRAEDTAVYYCARERNFRSGYSRYYYGMDV 115


RESULT 4
US-07-942-245-35
; Sequence 35, Application US/07942245
; Patent No. 5639641
;  GENERAL INFORMATION:
;    APPLICANT:  PEDERSEN, Jan T.
;    APPLICANT:  SEARLE,   Stephen M.J.
;    APPLICANT:  REES,     Anthony R.
;    APPLICANT:  ROGUSKA,  Michael A.
;    APPLICANT:  GUILD,    Braydon C.
;    TITLE OF INVENTION:  SURFACE RESIDUE VENEERING OF RODENT
;    TITLE OF INVENTION:  ANTIBODIES
;    NUMBER OF SEQUENCES:  522
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sughrue, Mion, Zinn, Macpeak & Seas
;      STREET:  2100 Pensylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  United States
;      ZIP:  20037-3202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  HP 9000/700 Workstation
;      OPERATING SYSTEM:  UNIX
;      SOFTWARE:  In house
;    CURRENT APPLICATION DATA:
```

```
;      APPLICATION NUMBER:  US/07/942,245
;      FILING DATE:  09-SEP-1992
;      CLASSIFICATION:  530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 293-7060
;      TELEFAX:  (202) 293-7860
;      TELEX:  6491103
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-942-245-35

  Query Match             86.3%;  Score 525;  DB 1;  Length 120;
  Best Local Similarity   91.1%;  Pred. No. 5.8e-47;
  Matches  102;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYG 112
              ||||||||||||||||||||||||||||||||||||||       : |:|
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRKDWGWALFDYWG 112


RESULT 5
US-09-240-274-25
; Sequence 25, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
;   LENGTH: 126
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain D30
US-09-240-274-25

  Query Match             86.3%;  Score 525;  DB 3;  Length 126;
  Best Local Similarity   85.2%;  Pred. No. 6.2e-47;
  Matches   98;  Conservative    9;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||:|||||||||||||||||||||||| | ||||||||||||||: ||||||:|
Db          1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYGMRWVRQAPGKGLEWVAVVYYDGSNKHY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              :|||||||||||||||||||:|||||||||||||||:|    :| : |||||||
Db         61 SDSVKGRFTISRDNSKNTLYLQMDSLRAEDTAVYYCARERNFRSGYSRYYYGMDV 115


RESULT 6
US-08-983-607-38
; Sequence 38, Application US/08983607
; Patent No. 6140470
;  GENERAL INFORMATION:
;    APPLICANT:  Alan Garen
;    APPLICANT:  Xiaohong Cai
;    TITLE OF INVENTION:  Human Anti-Tumor Monoclonal Anti-
;    TITLE OF INVENTION:  bodies
;    NUMBER OF SEQUENCES:  51
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Department of Molecular Biophysics
;      ADDRESSEE:  and Biochemistry, Yale University
;      STREET:  266 Whitney Avenue
;      CITY:  New Haven
;      STATE:  Connecticut
;      COUNTRY:  United States of America
;      ZIP:  06520-8114
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" 1.44 Mb diskette
;      COMPUTER:  IBM PC
;      OPERATING SYSTEM:  MS DOS
;      SOFTWARE:  Word Processing
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/983,607
;      FILING DATE:  April 27, 1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/IB96/01032
;      FILING DATE:  June 28, 1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mary M. Krinsky
;      REGISTRATION NUMBER:  32423
;      REFERENCE/DOCKET NUMBER:  OCR-679
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  203-773-9544
;      TELEFAX:  203-773-1183
;  INFORMATION FOR SEQ ID NO:  38:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 residues
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:
;      DESCRIPTION:  polypeptide
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens (melanoma patient
;      ORGANISM:  immunized with autologous tumor cells)
;      INDIVIDUAL ISOLATE:  peripheral blood lympho-
;      INDIVIDUAL ISOLATE:  cytes
;    IMMEDIATE SOURCE:
;      LIBRARY:  DM414 scFv antibodies obtained from
;      LIBRARY:  fUSE5 fusion phage construct
;      CLONE:  V575
;    FEATURE:
;      NAME/KEY:  heavy chain
US-08-983-607-38

  Query Match             86.2%;  Score 524;  DB 3;  Length 123;
  Best Local Similarity   92.2%;  Pred. No. 7.6e-47;
  Matches  107;  Conservative    0;  Mismatches    5;  Indels    4;  Gaps    3;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNS-KNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||| |||||||||||||||||||||  ||   |||   |||||
Db         61 ADSVKGRFTISRDNSKKNTLYLQMNSLRAEDTAVYYCA--RGFPYGGN-SDYGMDV 113


RESULT 7
US-09-726-219A-167
; Sequence 167, Application US/09726219A
; Patent No. 6806079
; GENERAL INFORMATION:
;  APPLICANT: Cambridge Antibody Technology
;  APPLICANT:  Cambridge Antibody Technology Limited
;  APPLICANT:  Medical Research Council
```

```
;  APPLICANT:  McCafferty, John
;  APPLICANT:  Pope, Anthony
;  APPLICANT:  Johnson, Kevin
;  APPLICANT:  Hoogenboom, Hendricus
;  APPLICANT:  Griffiths, Andrew
;  APPLICANT:  Jackson, Ronald
;  APPLICANT:  Holliger, Kasper
;  APPLICANT:  Marks, James
;  APPLICANT:  Clackson, Timothy
;  APPLICANT:  Chiswell, David
;  APPLICANT:  Winter, Gregory
;  APPLICANT:  Bonert, Timothy
;  TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
;  FILE REFERENCE: 213839-00013
;  CURRENT APPLICATION NUMBER: US/09/726,219A
;  CURRENT FILING DATE:  2000-11-28
;  PRIOR APPLICATION NUMBER: GB 9015198.6
;  PRIOR FILING DATE: 1990-07-10
;  PRIOR APPLICATION NUMBER: GB 9022845.3
;  PRIOR FILING DATE: 1990-10-19
;  PRIOR APPLICATION NUMBER: GB 9022845.3
;  PRIOR FILING DATE: 1990-10-19
;  PRIOR APPLICATION NUMBER: GB 9024503.6
;  PRIOR FILING DATE: 1990-11-12
;  PRIOR APPLICATION NUMBER: GB 9104744.9
;  PRIOR FILING DATE: 1991-03-06
;  PRIOR APPLICATION NUMBER: GB 9110549.4
;  PRIOR FILING DATE: 1991-05-15
;  PRIOR APPLICATION NUMBER: PCT/GB91/01134
;  PRIOR FILING DATE: 1991-07-10
;  PRIOR APPLICATION NUMBER: US 07/971,857
;  PRIOR FILING DATE: 1993-01-08
;  PRIOR APPLICATION NUMBER: US 08/484,893
;  PRIOR FILING DATE: 1995-06-07
;  NUMBER OF SEQ ID NOS: 272
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 167
;   LENGTH: 115
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-726-219A-167

  Query Match             85.4%;  Score 519;  DB 4;  Length 115;
  Best Local Similarity   89.4%;  Pred. No. 2.3e-46;
  Matches  101;  Conservative    5;  Mismatches    5;  Indels    2;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||:|||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          1 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYY-YYG 112
              |||||||||||||||||||||||||||||||:  | |:|  |: |:|
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK-TGYSSGWGYFDYWG 112


RESULT 8
US-08-211-202-141
; Sequence 141, Application US/08211202
; Patent No. 5565332
;  GENERAL INFORMATION:
;    APPLICANT:  HOOGENBOOM, Hendricus Renerus Jacobus Matteus
;    APPLICANT:  BAIER, Michael
;    APPLICANT:  JESPERS, Laurent Stephane Anne Therese
;    APPLICANT:  WINTER, Gregory Paul
;    TITLE OF INVENTION:  Production of  chimeric antibodies - a
;    TITLE OF INVENTION:  combinatorial approach
;    NUMBER OF SEQUENCES:  144
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David W. Clough, Marshall O'Toole Gerstein Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/211,202
;      FILING DATE:  23-SEP-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9120252.3
;      FILING DATE:  23-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9120377.8
;      FILING DATE:  25-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206318.9
;      FILING DATE:  24-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206372.6
;      FILING DATE:  24-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB92/00883
;      FILING DATE:  15-MAY-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  David W. Clough
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  28111/31960
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;      TELEFAX:  312-474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  141:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  116 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-211-202-141

  Query Match             85.2%;  Score 518;  DB 1;  Length 116;
  Best Local Similarity   89.5%;  Pred. No. 3e-46;
  Matches  102;  Conservative    2;  Mismatches    8;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAG--GNYYYYG 112
              |||||||||||||||||||||||||||||||||  |  | |    : |:|
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCASGRYCSGGSCSPFDYWG 114


RESULT 9
US-08-478-039-96
; Sequence 96, Application US/08478039
; Patent No. 5681722
;  GENERAL INFORMATION:
;    APPLICANT:  Newman, Roland A.
;    APPLICANT:  Hanna, Nabil
;    APPLICANT:  Raab, Ronald W.
;    TITLE OF INVENTION:  Recombinant Antibodies for Human Therapy
;    NUMBER OF SEQUENCES:  114
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;      STREET:  699 Prince St.
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
```

```
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/478,039
;       FILING DATE:  07-JUN-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/379,072
;       FILING DATE:  25-JAN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/912,292
;       FILING DATE:  10-JUL-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/856,281
;       FILING DATE:  23-MAR-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/735,064
;       FILING DATE:  25-JUL-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Teskin Esq., Robin L.
;       REGISTRATION NUMBER:  35,030
;       REFERENCE/DOCKET NUMBER:  012712-160
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  703-836-6620
;       TELEFAX:  703-836-2021
;   INFORMATION FOR SEQ ID NO:  96:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  128 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  not relevant
;       TOPOLOGY:  not relevant
;     MOLECULE TYPE:  peptide
;     POSITION IN GENOME:
;       CHROMOSOME/SEGMENT:  RF SJ2
US-08-478-039-96

  Query Match             84.8%;  Score 515.5;  DB 1;  Length 128;
  Best Local Similarity   87.3%;  Pred. No. 6e-46;
  Matches  103;  Conservative    1;  Mismatches   11;  Indels    3;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||| |||||||||||||||||||| ||||||||| ||||||||||
Db          1 QVQLVESGGGVVQPSRSLRLSCAASGFTFSSYAMHWVRGAPGKGLEWVXVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR---GISAGGNYYYYGMDV 115
              |||||||||||||:||||| |||||||||||||||||| |   | |    |||| |||
Db         61 ADSVKGRFTISRDDSKNTLSLQMNSLRAEDTAVYYCARGRFCSGQSCYSYYYYYYMDV 118


RESULT 10
US-08-476-349A-96
; Sequence 96, Application US/08476349A
; Patent No. 5750105
;  GENERAL INFORMATION:
;    APPLICANT:  Newman, Roland A.
;    APPLICANT:  Hanna, Nabil
;    APPLICANT:  Raab, Ronald W.
;    TITLE OF INVENTION:  Recombinant Antibodies for Human Therapy
;    NUMBER OF SEQUENCES:  114
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;      STREET:  699 Prince St.
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/476,349A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/379,072
;      FILING DATE:  25-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/912,292
;      FILING DATE:  10-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/856,281
;      FILING DATE:  23-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/735,064
;      FILING DATE:  25-JUL-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Teskin Esq., Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-161
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-836-6620
;      TELEFAX:  703-836-2021
;  INFORMATION FOR SEQ ID NO:  96:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  128 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  peptide
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:  RF SJ2
US-08-476-349A-96

  Query Match             84.8%;  Score 515.5;  DB 1;  Length 128;
  Best Local Similarity   87.3%;  Pred. No. 6e-46;
  Matches  103;  Conservative    1;  Mismatches   11;  Indels    3;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||| |||||||||||||||||||| ||||||||| ||||||||||
Db          1 QVQLVESGGGVVQPSRSLRLSCAASGFTFSSYAMHWVRGAPGKGLEWVXVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR---GISAGGNYYYYGMDV 115
              |||||||||||||:||||| |||||||||||||||||| |   | |    |||| |||
Db         61 ADSVKGRFTISRDDSKNTLSLQMNSLRAEDTAVYYCARGRFCSGQSCYSYYYYYYMDV 118


RESULT 11
US-09-424-840B-6
; Sequence 6, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
;  APPLICANT: Berchtold, Peter
;  APPLICANT:  Escher, Robert F. A.
;  TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
;  FILE REFERENCE: 100564-09049
;  CURRENT APPLICATION NUMBER: US/09/424,840B
;  CURRENT FILING DATE:  1999-12-03
;  PRIOR APPLICATION NUMBER: DE 19820663.1
;  PRIOR FILING DATE: 1998-05-08
;  PRIOR APPLICATION NUMBER: DE 19755227.7
;  PRIOR FILING DATE: 1997-12-12
;  PRIOR APPLICATION NUMBER: DE 19723904.8
;  PRIOR FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 128
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-424-840B-6

  Query Match             84.6%;  Score 514.5;  DB 4;  Length 123;
```

```
  Best Local Similarity   87.8%;  Pred. No. 7.3e-46;
  Matches  101;  Conservative    4;  Mismatches    7;  Indels    3;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||:|:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVKLLESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||| |||||||||||||||||||||||||  |   | ::|   |||
Db         61 ADSVKGRFAISRDNSKNTLYLQMNSLRAEDTAVYYCARALGSWGGWDHY---MDV 112


RESULT 12
US-08-331-398A-46
; Sequence 46, Application US/08331398A
; Patent No. 5608039
;  GENERAL INFORMATION:
;    APPLICANT:  Pastan, Ira
;    APPLICANT:  Willingham, Mark
;    APPLICANT:  FitzGerald, David
;    APPLICANT:  Brinkmann, Ulrich
;    APPLICANT:  Pai, Lee
;    TITLE OF INVENTION:  Single Chain B3 Antibody Fusion Proteins
;    TITLE OF INVENTION:  and Their Uses (as amended)
;    NUMBER OF SEQUENCES:  68
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  One Market Plaza, Steuart Street Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105-1492
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/331,398A
;      FILING DATE:  28-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/767,331
;      FILING DATE:  30-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/596,289
;      FILING DATE:  12-OCT-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  015280-126110US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 543-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..119
;      OTHER INFORMATION:  /note= "Human fetal immunoglobulin
;      OTHER INFORMATION:  56P1'CL Variable Heavy chain (V-H)"
US-08-331-398A-46

  Query Match             84.4%;  Score 513;  DB 1;  Length 119;
  Best Local Similarity   88.6%;  Pred. No. 1e-45;
  Matches  101;  Conservative    3;  Mismatches    4;  Indels    6;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVELVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYY--YYG 112
              |||||||||||||||||||||||||||||||||||||||     :   ||  |:|
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR----RSARTYYFDYWG 110


RESULT 13
US-08-331-397B-46
; Sequence 46, Application US/08331397B
; Patent No. 5981726
;  GENERAL INFORMATION:
;    APPLICANT:  Pastan, Ira
;    APPLICANT:  Benhar, Itai
;    TITLE OF INVENTION:  Chimeric and Mutationally Stabilized Tumor-
;    TITLE OF INVENTION:  Specific Antibody Fragments, Fusion Proteins, and Uses
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  68
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  One Market Plaza, Steuart Street Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105-1492
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/331,397B
;      FILING DATE:  28-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/767,331
;      FILING DATE:  30-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/596,289
;      FILING DATE:  12-OCT-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  015280-126120US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 543-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..119
;      OTHER INFORMATION:  /note= "Human fetal immunoglobulin
;      OTHER INFORMATION:  56P1'CL Variable Heavy chain (V-H)"
US-08-331-397B-46

  Query Match             84.4%;  Score 513;  DB 2;  Length 119;
  Best Local Similarity   88.6%;  Pred. No. 1e-45;
  Matches  101;  Conservative    3;  Mismatches    4;  Indels    6;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVELVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYY--YYG 112
              |||||||||||||||||||||||||||||||||||||||     :   ||  |:|
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR----RSARTYYFDYWG 110
```

```
RESULT 14
US-08-759-804A-46
; Sequence 46, Application US/08759804A
; Patent No. 5990296
;  GENERAL INFORMATION:
;    APPLICANT:  Pastan, Ira
;    APPLICANT:  Willingham, Mark
;    APPLICANT:  FitzGerald, David J.
;    APPLICANT:  Brinkmann, Ulrich
;    APPLICANT:  Pai, Lee
;    TITLE OF INVENTION:  Tumor-Specific Antibody Fragments,
;    TITLE OF INVENTION:  Fusion Proteins, and Uses Thereof
;    NUMBER OF SEQUENCES:  68
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/759,804A
;      FILING DATE:  03-DEC-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/331,398
;      FILING DATE:  28-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/767,331
;      FILING DATE:  30-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/596,289
;      FILING DATE:  12-OCT-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weber, Ellen L.
;      REGISTRATION NUMBER:  32,762
;      REFERENCE/DOCKET NUMBER:  015280-126140US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..119
;      OTHER INFORMATION:  /note= "Human fetal immunoglobulin
;      OTHER INFORMATION:  56P1'CL Variable Heavy chain (V-H)"
US-08-759-804A-46

  Query Match             84.4%;  Score 513;  DB 2;  Length 119;
  Best Local Similarity   88.6%;  Pred. No. 1e-45;
  Matches  101;  Conservative    3;  Mismatches    4;  Indels    6;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVELVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYY--YYG 112
              ||||||||||||||||||||||||||||||||||||     :   ||  |:|
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR----RSARTYYFDYWG 110
```

```
RESULT 15
US-09-227-693-46
; Sequence 46, Application US/09227693
; Patent No. 6287562
;  GENERAL INFORMATION:
;    APPLICANT:  PASTAN, Ira
;    APPLICANT:  BENHAR, Itai
;    APPLICANT:  PADLAN, Eduardo A.
;    APPLICANT:  JUNG, Sun-Hee
;    APPLICANT:  LEE, Byungkook
;    TITLE OF INVENTION:  HUMANIZED TUMOR-SPECIFIC ANTIBODY
;    TITLE OF INVENTION:  FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
;    NUMBER OF SEQUENCES:  50
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  Steuart Street Tower, One Market Plaza
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94105-1493
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/227,693
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/331,396
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/767,331
;      FILING DATE:  30-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/596,289
;      FILING DATE:  12-OCT-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weber, Ellen Lauver
;      REGISTRATION NUMBER:  32,762
;      REFERENCE/DOCKET NUMBER:  15280-126-1-3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 543-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..119
;      OTHER INFORMATION:  /note= "Human fetal immunoglobulin
;      OTHER INFORMATION:  56P1'CL VH region"
US-09-227-693-46

  Query Match             84.4%;  Score 513;  DB 3;  Length 119;
  Best Local Similarity   88.6%;  Pred. No. 1e-45;
  Matches  101;  Conservative    3;  Mismatches    4;  Indels    6;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVELVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYY--YYG 112
              ||||||||||||||||||||||||||||||||||||     :   ||  |:|
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR----RSARTYYFDYWG 110


RESULT 16
```

```
US-08-211-202-118
; Sequence 118, Application US/08211202
; Patent No. 5565332
;  GENERAL INFORMATION:
;    APPLICANT:  HOOGENBOOM, Hendricus Renerus Jacobus Matteus
;    APPLICANT:  BAIER, Michael
;    APPLICANT:  JESPERS, Laurent Stephane Anne Therese
;    APPLICANT:  WINTER, Gregory Paul
;    TITLE OF INVENTION:  Production of  chimeric antibodies - a
;    TITLE OF INVENTION:  combinatorial approach
;    NUMBER OF SEQUENCES:  144
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David W. Clough, Marshall O'Toole Gerstein Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/211,202
;      FILING DATE:  23-SEP-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9120252.3
;      FILING DATE:  23-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9120377.8
;      FILING DATE:  25-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206318.9
;      FILING DATE:  24-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206372.6
;      FILING DATE:  24-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB92/00883
;      FILING DATE:  15-MAY-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  David W. Clough
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  28111/31960
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;      TELEFAX:  312-474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  118:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  98 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-211-202-118

  Query Match             84.2%;  Score 512;  DB 1;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 1e-45;
  Matches   98;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR 98
              ||||||||||||||||||||||||||||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR 98


RESULT 17
US-09-315-926A-80
; Sequence 80, Application US/09315926A
; Patent No. 6498027
; GENERAL INFORMATION:
;  APPLICANT: Es van, Helmuth
;  APPLICANT:  Havenga, Menzo
;  APPLICANT:  Verlinden, Stefan
;  TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
;  FILE REFERENCE: 2183-4080US
;  CURRENT APPLICATION NUMBER: US/09/315,926A
;  CURRENT FILING DATE:  1999-05-20
;  PRIOR APPLICATION NUMBER: EP 99201593.3
;  PRIOR FILING DATE: 1999-05-20
;  PRIOR APPLICATION NUMBER: EP 98201693.3
;  PRIOR FILING DATE: 1998-05-20
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
;   LENGTH: 248
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Description of Artificial Sequence: phage
;   NAME/KEY: PEPTIDE
;   LOCATION: (1)..(248)
;   OTHER INFORMATION: /note="hCAT1 amino acid sequence"
US-09-315-926A-80

  Query Match             84.1%;  Score 511.5;  DB 4;  Length 248;
  Best Local Similarity   89.4%;  Pred. No. 3.4e-45;
  Matches  101;  Conservative    4;  Mismatches    5;  Indels    3;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 82

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGIS-AGGNYYYYG 112
              |||||||||||||||||||||||||||||||||||||||||  |||:    : |:|
Db         83 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA--RGITVTKSRFDYWG 133


RESULT 18
US-09-079-029-11
; Sequence 11, Application US/09079029
; Patent No. 6342369
;  GENERAL INFORMATION:
;    APPLICANT:  Adams, Camilia W.
;    APPLICANT:  Ashkenazi, Avi J.
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Kim, Kyung J.
;    TITLE OF INVENTION:  Apo-2 Receptor
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,029
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marschang, Diane L.
;      REGISTRATION NUMBER:  35,600
;      REFERENCE/DOCKET NUMBER:  P1101R2
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5416
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  310 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-079-029-11

  Query Match             84.0%;  Score 511;  DB 3;  Length 310;
  Best Local Similarity   87.0%;  Pred. No. 5e-45;
  Matches  100;  Conservative    1;  Mismatches    6;  Indels    8;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||:|||||||||||||||||||| |||| |||||||||||||| | ||| ||||
Db         40 QVQLVQSGGGVVQPGRSLRLSCAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYY 99

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||||||||        || |||
Db        100 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRG--------YYYMDV 146


RESULT 19
US-09-025-769B-24
; Sequence 24, Application US/09025769B
; Patent No. 6300064
;  GENERAL INFORMATION:
;    APPLICANT:  Knappik, Achim
;    APPLICANT:  Pack, Peter
;    APPLICANT:  Ilag, Vic
;    APPLICANT:  Ge, Liming
;    APPLICANT:  Moroney, Simon
;    APPLICANT:  Plueckthun, Andreas
;    TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES:  373
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  James F. Haley, Jr., Esq. c/o Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10021
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/025,769B
;      FILING DATE:  18-FEB-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95 11 3021.0
;      FILING DATE:  18-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  James F. Haley, Jr., Esq.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  MORPHO/5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)596-9000
;      TELEFAX:  (212)596-9090
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  117 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-025-769B-24

  Query Match             83.9%;  Score 510;  DB 3;  Length 117;
  Best Local Similarity   87.5%;  Pred. No. 2e-45;
  Matches   98;  Conservative    5;  Mismatches    7;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||||||||:|||| |||||||||||||||||||||||||||||:|||||| | ||
Db          1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVSVISYDGGNTYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYG 112
              |||||||||||||||||||||||||||||||||||||||||    |:|:  |
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRG--GSGDYWGQG 110


RESULT 20
US-09-490-070A-24
; Sequence 24, Application US/09490070A
; Patent No. 6696248
;  GENERAL INFORMATION:
;       APPLICANT: Knappik, Achim
;                  Pack, Peter
;                  Ilag, Vic
;                  Ge, Liming
;                  Moroney, Simon
;                  Plueckthun, Andreas
;       TITLE OF INVENTION: Protein/(Poly)peptide libraries
;       NUMBER OF SEQUENCES: 373
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
;                       White & McAuliffe
;            STREET: 1666 K Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20006
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/490,070A
;            FILING DATE: 24-Jan-2000
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: EP 95 11 3021.0
;            FILING DATE: 18-AUG-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Colin G. Sandercock, Esq.
;            REGISTRATION NUMBER: 31,298
;            REFERENCE/DOCKET NUMBER: 37629-0005
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202) 912-2000
;            TELEFAX: (202) 912-2020
;  INFORMATION FOR SEQ ID NO: 24:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 117 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-490-070A-24

  Query Match             83.9%;  Score 510;  DB 4;  Length 117;
  Best Local Similarity   87.5%;  Pred. No. 2e-45;
  Matches   98;  Conservative    5;  Mismatches    7;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||||||||:|||| |||||||||||||||||||||||||||||:|||||| | ||
Db          1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVSVISYDGGNTYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYG 112
              |||||||||||||||||||||||||||||||||||||||||    |:|:  |
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRG--GSGDYWGQG 110


RESULT 21
```

```
US-09-490-153-24
; Sequence 24, Application US/09490153
; Patent No. 6706484
;  GENERAL INFORMATION:
;       APPLICANT: Knappik, Achim
;                  Pack, Peter
;                  Ilag, Vic
;                  Ge, Liming
;                  Moroney, Simon
;                  Plueckthun, Andreas
;       TITLE OF INVENTION: Protein/(Poly)peptide libraries
;       NUMBER OF SEQUENCES: 373
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;            STREET: 1251 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10021
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/490,153
;            FILING DATE: 24-Jan-2000
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/025,769B
;            FILING DATE: 18-FEB-1998
;            APPLICATION NUMBER: EP 95 11 3021.0
;            FILING DATE: 18-AUG-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: James F. Haley, Jr., Esq.
;            REGISTRATION NUMBER: 27,794
;            REFERENCE/DOCKET NUMBER: MORPHO/5
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212)596-9000
;            TELEFAX: (212)596-9090
;   INFORMATION FOR SEQ ID NO: 24:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 117 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-490-153-24

  Query Match             83.9%;  Score 510;  DB 4;  Length 117;
  Best Local Similarity   87.5%;  Pred. No. 2e-45;
  Matches   98;  Conservative    5;  Mismatches    7;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||||||||:|||| ||||||||||||||||||||||||||||:|||||| | ||
Db          1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVSVISYDGGNTYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYG 112
              |||||||||||||||||||||||||||||||||||||||    |:|:  |
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRG--GSGDYWGQG 110


RESULT 22
US-09-490-324-24
; Sequence 24, Application US/09490324
; Patent No. 6828422
;  GENERAL INFORMATION:
;       APPLICANT: Knappik, Achim
;                  Pack, Peter
;                  Ilag, Vic
;                  Ge, Liming
;                  Moroney, Simon
;                  Plueckthun, Andreas
;       TITLE OF INVENTION: Protein/(Poly)peptide libraries
;       NUMBER OF SEQUENCES: 373
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;            STREET: 1251 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10021
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/490,324
;            FILING DATE: 24-Jan-2000
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/025,769
;            FILING DATE: 18-FEB-1998
;            APPLICATION NUMBER: EP 95 11 3021.0
;            FILING DATE: 18-AUG-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: James F. Haley, Jr., Esq.
;            REGISTRATION NUMBER: 27,794
;            REFERENCE/DOCKET NUMBER: MORPHO/5
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212)596-9000
;            TELEFAX: (212)596-9090
;   INFORMATION FOR SEQ ID NO: 24:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 117 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-490-324-24

  Query Match             83.9%;  Score 510;  DB 4;  Length 117;
  Best Local Similarity   87.5%;  Pred. No. 2e-45;
  Matches   98;  Conservative    5;  Mismatches    7;  Indels    2;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||||||||:|||| ||||||||||||||||||||||||||||:|||||| | ||
Db          1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVSVISYDGGNTYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYG 112
              |||||||||||||||||||||||||||||||||||||||    |:|:  |
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRG--GSGDYWGQG 110


RESULT 23
US-08-545-809A-115
; Sequence 115, Application US/08545809A
; Patent No. 6096878
;  GENERAL INFORMATION:
;    APPLICANT:  Honjo, Tasuku
;    APPLICANT:  Matsuda, Fumihiko
;    TITLE OF INVENTION:  HUMAN IMMUNOGLOBULIN VH GENE
;    TITLE OF INVENTION:  SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
;    NUMBER OF SEQUENCES:  145
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
```

```
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/545,809A
;      FILING DATE:  27-MAR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP93/00603
;      FILING DATE:  10-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Freeman, John W.
;      REGISTRATION NUMBER:  29,066
;      REFERENCE/DOCKET NUMBER:  06501/004001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542-5070
;      TELEFAX:  617-542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  115:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  117 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-545-809A-115

  Query Match           83.6%;  Score 508;  DB 3;  Length 117;
  Best Local Similarity   99.0%;  Pred. No. 3.2e-45;
  Matches   97;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db         20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR 98
              ||||||||||||||||||||||||||||||||||||||
Db         80 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR 117


RESULT 24
US-09-424-840B-16
; Sequence 16, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
;  APPLICANT: Berchtold, Peter
;  APPLICANT:  Escher, Robert F. A.
;  TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
;  FILE REFERENCE: 100564-09049
;  CURRENT APPLICATION NUMBER: US/09/424,840B
;  CURRENT FILING DATE:  1999-12-03
;  PRIOR APPLICATION NUMBER: DE 19820663.1
;  PRIOR FILING DATE: 1998-05-08
;  PRIOR APPLICATION NUMBER: DE 19755227.7
;  PRIOR FILING DATE: 1997-12-12
;  PRIOR APPLICATION NUMBER: DE 19723904.8
;  PRIOR FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 128
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 124
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-424-840B-16

  Query Match           82.6%;  Score 502;  DB 4;  Length 124;
  Best Local Similarity   84.5%;  Pred. No. 1.4e-44;
  Matches   98;  Conservative    6;  Mismatches    8;  Indels    4;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||:|:||||||| ||||||||||||||||| ||||||||||||:||||||||||
Db          1 QVKLLESGGGVVHPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVALISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYY-GMDV 115
              |||||||| |||||||||||||||||||||||||:|      |:|  : |||| |||
Db         61 ADSVKGRFAISRDNSKNTLYLQMNSLRAEDTAVYYCAKD---GRSGSYARFDGMDV 113


RESULT 25
US-08-211-202-135
; Sequence 135, Application US/08211202
; Patent No. 5565332
;  GENERAL INFORMATION:
;    APPLICANT:  HOOGENBOOM, Hendricus Renerus Jacobus Matteus
;    APPLICANT:  BAIER, Michael
;    APPLICANT:  JESPERS, Laurent Stephane Anne Therese
;    APPLICANT:  WINTER, Gregory Paul
;    TITLE OF INVENTION:  Production of  chimeric antibodies - a
;    TITLE OF INVENTION:  combinatorial approach
;    NUMBER OF SEQUENCES:  144
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David W. Clough, Marshall O'Toole Gerstein Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/211,202
;      FILING DATE:  23-SEP-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9120252.3
;      FILING DATE:  23-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9120377.8
;      FILING DATE:  25-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206318.9
;      FILING DATE:  24-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206372.6
;      FILING DATE:  24-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB92/00883
;      FILING DATE:  15-MAY-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  David W. Clough
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  28111/31960
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;      TELEFAX:  312-474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  135:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-211-202-135

  Query Match           82.4%;  Score 501;  DB 1;  Length 120;
  Best Local Similarity   89.1%;  Pred. No. 1.8e-44;
  Matches   98;  Conservative    4;  Mismatches    4;  Indels    4;  Gaps    2;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||| |||||:|:|| ||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLQESGGGLVKPGGSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYY 110
              |||||||||||||||||||||||||||||||||:  |:   | |||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKG-GL---GTYYY 106
```

Search completed: June 16, 2005, 07:44:03
Job time : 33.4574 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 07:35:01 ; Search time 121.188 Seconds
(without alignments)
367.011 Million cell updates/sec

Title: US-09-920-137D-7
Perfect score: 608
Sequence: 1 QVQLVESGGGVVQPGRSLRL.....CARDRGISAGGNYYYYGMDV 115

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	608	100.0	115	5	AAM51164	Aam51164 Anti-tumo
2	577	94.9	115	7	ADJ73536	Adj73536 Erythropo
3	577	94.9	115	7	ADJ73540	Adj73540 Erythropo
4	572	94.1	133	7	ADJ73535	Adj73535 Erythropo
5	571.5	94.0	146	5	AAM51169	Aam51169 Human rec
6	569.5	93.7	146	5	AAM51168	Aam51168 Human rec
7	566.5	93.2	146	5	AAM51171	Aam51171 Human rec
8	561.5	92.4	146	5	AAM51170	Aam51170 Human rec
9	561.5	92.4	146	5	AAM51172	Aam51172 Human rec
10	553	91.0	124	6	ADA89238	Ada89238 Human ant
11	550.5	90.5	127	2	AAY17954	Aay17954 Human D4.
12	550.5	90.5	138	2	AAW80815	Aaw80815 Amino aci
13	550.5	90.5	252	5	ABP45720	Abp45720 Human BLy
14	550.5	90.5	252	7	ADG96547	Adg96547 Single ch
15	550.5	90.5	523	3	AAY44994	Aay44994 HD70scFv-
16	550.5	90.5	524	3	AAY44995	Aay44995 HD70scFv-
17	550	90.5	126	7	ADK18593	Adk18593 Anti-huma
18	550	90.5	126	7	ADK18785	Adk18785 Anti-huma
19	550	90.5	126	7	ADK18858	Adk18858 Anti-huma
20	550	90.5	126	8	ADL25404	Adl25404 Human mAb
21	546	89.8	126	8	ADP22222	Adp22222 Human ant
22	545.5	89.7	125	8	ADP22300	Adp22300 Human ant
23	545.5	89.7	125	8	ADP22316	Adp22316 Human ant
24	545.5	89.7	125	8	ADP22312	Adp22312 Human ant
25	545	89.6	118	5	AAM51167	Aam51167 Human DP-
26	544	89.5	122	8	ADR38664	Adr38664 Mouse hea
27	543	89.3	126	7	ADK18786	Adk18786 Anti-huma
28	543	89.3	126	7	ADK18822	Adk18822 Anti-huma
29	543	89.3	126	7	ADK18882	Adk18882 Anti-huma
30	543	89.3	126	7	ADK18601	Adk18601 Anti-huma
31	543	89.3	126	8	ADL25420	Adl25420 Human mAb
32	542.5	89.2	451	3	AAY93734	Aay93734 The heavy
33	542.5	89.2	451	6	AAE35889	Aae35889 Human 11.
34	542	89.1	122	8	ADR38663	Adr38663 Mouse hea
35	541	89.0	122	8	ADP22128	Adp22128 Human ant
36	541	89.0	126	7	ADK18821	Adk18821 Anti-huma
37	540.5	88.9	123	8	ADS84372	Ads84372 Human ant
38	540.5	88.9	123	8	ADR68514	Adr68514 Anti-EPO-
39	540.5	88.9	125	7	ADE28451	Ade28451 Human ant
40	540.5	88.9	470	7	ADE28475	Ade28475 Human ant
41	540	88.8	134	8	ADP22348	Adp22348 Human ant
42	539	88.7	131	7	ADJ73539	Adj73539 Erythropo
43	537.5	88.4	123	8	ADS84396	Ads84396 Human ant
44	537.5	88.4	123	8	ADR68538	Adr68538 Anti-EPO-
45	536.5	88.2	123	8	ADS84376	Ads84376 Human ant
46	536.5	88.2	123	8	ADS84368	Ads84368 Human ant
47	536.5	88.2	123	8	ADR68518	Adr68518 Anti-EPO-
48	536.5	88.2	123	8	ADR68510	Adr68510 Anti-EPO-
49	536.5	88.2	125	8	ADP22268	Adp22268 Human ant
50	536.5	88.2	125	8	ADP22198	Adp22198 Human ant
51	535.5	88.1	125	8	ADP22100	Adp22100 Human ant
52	534	87.8	124	8	ADP22136	Adp22136 Human ant
53	534	87.8	249	5	ABP44501	Abp44501 Human BLy
54	534	87.8	249	7	ADG95328	Adg95328 Single ch
55	533	87.7	126	4	AAG93583	Aag93583 Human ant
56	533	87.7	126	6	ABO27390	Abo27390 Anti-Rh(D
57	532.5	87.6	123	8	ADP22218	Adp22218 Human ant
58	532.5	87.6	127	7	ADP03980	Adp03980 Murine-ex
59	532.5	87.6	144	6	AAE37209	Aae37209 Human AB-
60	531	87.3	126	7	ADP03963	Adp03963 Murine-ex
61	529.5	87.1	123	8	ADP22226	Adp22226 Human ant
62	528.5	86.9	252	5	ABP45383	Abp45383 Human BLy
63	528.5	86.9	252	7	ADG96210	Adg96210 Single ch
64	527	86.7	117	8	ADO36345	Ado36345 Intracell
65	527	86.7	119	7	ADL91318	Adl91318 VH chain
66	527	86.7	126	4	AAG93641	Aag93641 Human ant
67	527	86.7	126	6	ABO27448	Abo27448 Anti-Rh(D
68	527	86.7	254	5	ABP44970	Abp44970 Human BLy
69	527	86.7	254	7	ADG95797	Adg95797 Single ch
70	526.5	86.6	125	8	ADP22156	Adp22156 Human ant
71	526.5	86.6	125	8	ADP22152	Adp22152 Human ant
72	526	86.5	120	7	ADC99800	Adc99800 Anti-huma
73	526	86.5	120	7	ADD05404	Add05404 Anti-MUC1
74	526	86.5	120	7	ADF09842	Adf09842 Human ant
75	526	86.5	247	5	ABP45319	Abp45319 Human BLy
76	526	86.5	247	7	ADG96146	Adg96146 Single ch
77	526	86.5	249	5	ABP45713	Abp45713 Human BLy
78	526	86.5	249	5	ABP45714	Abp45714 Human BLy
79	526	86.5	249	7	ADG96540	Adg96540 Single ch
80	526	86.5	249	7	ADG96541	Adg96541 Single ch
81	526	86.5	256	5	ABP44828	Abp44828 Human BLy
82	526	86.5	256	7	ADG95655	Adg95655 Single ch
83	525.5	86.4	121	7	ADP03962	Adp03962 Murine-ex
84	525	86.3	120	2	AAR52064	Aar52064 Heavy cha
85	525	86.3	126	4	AAG93582	Aag93582 Human ant
86	525	86.3	126	6	ABO27389	Abo27389 Anti-Rh(D
87	525	86.3	143	3	AAY82629	Aay82629 Human PTH
88	524.5	86.3	125	7	ADE28443	Ade28443 Human ant
89	524.5	86.3	470	7	ADE28467	Ade28467 Human ant
90	524	86.2	123	2	AAW13531	Aaw13531 Anti-mela
91	523	86.0	143	6	AAE37203	Aae37203 Human AB-
92	523	86.0	249	5	ABP45091	Abp45091 Human BLy
93	523	86.0	249	5	ABP45104	Abp45104 Human BLy
94	523	86.0	249	5	ABP44386	Abp44386 Human BLy
95	523	86.0	249	7	ADG95213	Adg95213 Single ch
96	523	86.0	249	7	ADG95918	Adg95918 Single ch
97	523	86.0	249	7	ADG95931	Adg95931 Single ch
98	522.5	85.9	142	6	AAE37201	Aae37201 Human AB-

99	522	85.9	124	8	ADP22132	Adp22132 Human ant
100	521	85.7	128	8	ADP22160	Adp22160 Human ant

ALIGNMENTS

RESULT 1
AAM51164
ID AAM51164 standard; protein; 115 AA.
XX
AC AAM51164;
XX
DT 10-JUN-2002 (first entry)
XX
DE Anti-tumour necrosis factor antibody heavy chain variable region.
XX
KW Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;
KW complementarity determining region; antirheumatic; antiarthritic;
KW antiulcer; antiasthmatic; antiallergic; antiinflammatory; antisickling;
KW antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;
KW antianginal; cardiant; antibacterial; virucide; fungicide; antileprotic;
KW protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;
KW human; diagnosis; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1. .30
FT /label= FR1
FT Region 31. .35
FT /label= CDR1
FT Region 36. .49
FT /label= FR2
FT Region 50. .66
FT /label= CDR2
FT Region 67. .98
FT /label= FR3
FT Region 99. .107
FT /label= CDR3
FT Region 108. .115
FT /label= J6
XX
PN WO200212502-A2.
XX
PD 14-FEB-2002.
XX
PF 07-AUG-2001; 2001WO-US024785.
XX
PR 07-AUG-2000; 2000US-0223360P.
PR 29-SEP-2000; 2000US-0236826P.
PR 01-AUG-2001; 2001US-00920137.
XX
PA (CENZ) CENTOCOR INC.
XX
PI Giles-Komar J, Knight DM, Heavner G, Scallon B, Shealy D;
XX
DR WPI; 2002-217194/27.
XX
PT Novel isolated mammalian anti-tumor necrosis factor antibody, useful for
PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,
PT angina pectoris, myocardial infarction, leprosy.
XX
PS Claim 9; Page 129; 131pp; English.
XX
CC The present sequence is that of the heavy chain variable region of an
CC anti-tumour necrosis factor (TNF) antibody of the invention. The
CC invention provides isolated human, primate, rodent, mammalian, chimeric,
CC humanised and/or complementarity determining region (CDR)-grafted anti-
CC TNF antibodies, immunoglobulins, cleavage products and other specified
CC portions and variants, as well as anti-TNF antibody compositions,
CC encoding or complementary nucleic acids, vectors, host cells,
CC compositions, formulations, devices, transgenic animals, transgenic
CC plants, and methods of making and using them. The anti-TNF antibody
CC comprises at least a portion of an immunoglobulin molecule, especially
CC the heavy chain and/or light chain variable regions given in the present
CC sequence and in AAM51165, or either all of the CDRs of the heavy chain
CC (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-
CC 63). The antibody may inhibit TNF-induced cell adhesion molecules,
CC inhibit TNF binding to receptor, or provide Arthritic Index improvement
CC in a mouse model. It is useful for diagnosing or treating a TNF related
CC condition in a cell, tissue, organ or animal (claimed) such as rheumatoid
CC arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology,
CC sickle cell anaemia, diabetes, a cardiovascular disease such as
CC arteriosclerosis, atherosclerosis, restenosis, angina pectoris or
CC myocardial infarction, an infectious disease in a cell such as bacterial,
CC viral, and fungal infections, pneumonia, leprosy and malaria, a malignant
CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
CC lymphoma and multiple myeloma, or a neurological disease such as multiple
CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and
CC Creutzfeldt-Jakob disease
XX
SQ Sequence 115 AA;

Query Match 100.0%; Score 608; DB 5; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.5e-48;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
```

RESULT 2
ADJ73536
ID ADJ73536 standard; protein; 115 AA.
XX
AC ADJ73536;
XX
DT 06-MAY-2004 (first entry)
XX
DE Erythropoietin heavy chain mimetibody SeqID 992.
XX
KW mimetic; CDR mimetibody; gene therapy; transgenic; immune;
KW cardiovascular; infectious; malignant; neurologic disease; anaemia;
KW immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
KW erythropoietin.
XX
OS Synthetic.
XX
PN WO2003084477-A2.
XX
PD 16-OCT-2003.
XX
PF 24-MAR-2003; 2003WO-US009139.
XX
PR 29-MAR-2002; 2002US-0368791P.
XX
PA (CENZ) CENTOCOR INC.
XX
PI Heavner GA, Knight DM, Scallon BJ, Ghrayeb J;
XX
DR WPI; 2003-804237/75.
XX
PT New CDR mimetibody comprising a portion of a heavy or light chain
PT variable region comprising human framework or ligand binding region,
PT useful for preparing a composition for treating e.g., immune,
PT cardiovascular or neurologic disease.
XX
PS Example 2; SEQ ID NO 992; 97pp; English.
XX
CC This invention relates to novel mammalian CDR mimetibodies, specific

CC portions or variants thereof. Specifically, it refers to an antibody
CC fragment where a protein has been inserted into, or replaces a portion
CC of, one or more CDR regions, such that each CDR mimetibody comprises at
CC least one portion of a heavy chain or light chain variable region, which
CC itself comprises at least one human framework region and at least one
CC ligand binding region (LBR). The present invention describes human
CC mimetibodies, including modified immunoglobulins and cleavage products
CC that can be useful in gene therapy and the generation of transgenic
CC plants and animals. Furthermore, the CDR mimetibody is useful for
CC preparing compositions for modulating, treating or reducing the symptoms
CC of immune, cardiovascular, infectious, malignant and/ or neurologic
CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This
CC polypeptide sequence is an erythropoietin heavy chain mimetibody of the
CC invention.
XX
SQ Sequence 115 AA;

Query Match 94.9%; Score 577; DB 7; Length 115;
Best Local Similarity 95.7%; Pred. No. 1.8e-45;
Matches 110; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
Db 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
Db 61 ADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGIGGWQNYYYYGMDV 115

RESULT 3
ADJ73540
ID ADJ73540 standard; protein; 115 AA.
XX
AC ADJ73540;
XX
DT 06-MAY-2004 (first entry)
XX
DE Erythropoietin heavy chain mimetibody SeqID 996.
XX
KW mimetic; CDR mimetibody; gene therapy; transgenic; immune;
KW cardiovascular; infectious; malignant; neurologic disease; anaemia;
KW immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
KW erythropoietin.
XX
OS Synthetic.
XX
PN WO2003084477-A2.
XX
PD 16-OCT-2003.
XX
PF 24-MAR-2003; 2003WO-US009139.
XX
PR 29-MAR-2002; 2002US-0368791P.
XX
PA (CENZ) CENTOCOR INC.
XX
PI Heavner GA, Knight DM, Scallon BJ, Ghrayeb J;
XX
DR WPI; 2003-804237/75.
XX
PT New CDR mimetibody comprising a portion of a heavy or light chain
PT variable region comprising human framework or ligand binding region,
PT useful for preparing a composition for treating e.g., immune,
PT cardiovascular or neurologic disease.
XX
PS Example 2; SEQ ID NO 996; 97pp; English.
XX
CC This invention relates to novel mammalian CDR mimetibodies, specific
CC portions or variants thereof. Specifically, it refers to an antibody
CC fragment where a protein has been inserted into, or replaces a portion
CC of, one or more CDR regions, such that each CDR mimetibody comprises at
CC least one portion of a heavy chain or light chain variable region, which
CC itself comprises at least one human framework region and at least one
CC ligand binding region (LBR). The present invention describes human
CC mimetibodies, including modified immunoglobulins and cleavage products
CC that can be useful in gene therapy and the generation of transgenic
CC plants and animals. Furthermore, the CDR mimetibody is useful for
CC preparing compositions for modulating, treating or reducing the symptoms
CC of immune, cardiovascular, infectious, malignant and/ or neurologic
CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This
CC polypeptide sequence is an erythropoietin heavy chain mimetibody of the
CC invention.
XX
SQ Sequence 115 AA;

Query Match 94.9%; Score 577; DB 7; Length 115;
Best Local Similarity 95.7%; Pred. No. 1.8e-45;
Matches 110; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
Db 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
Db 61 ADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGIGGWQNYYYYGMDV 115

RESULT 4
ADJ73535
ID ADJ73535 standard; protein; 133 AA.
XX
AC ADJ73535;
XX
DT 06-MAY-2004 (first entry)
XX
DE Erythropoietin heavy chain mimetibody SeqID 991.
XX
KW mimetic; CDR mimetibody; gene therapy; transgenic; immune;
KW cardiovascular; infectious; malignant; neurologic disease; anaemia;
KW immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
KW erythropoietin.
XX
OS Synthetic.
XX
PN WO2003084477-A2.
XX
PD 16-OCT-2003.
XX
PF 24-MAR-2003; 2003WO-US009139.
XX
PR 29-MAR-2002; 2002US-0368791P.
XX
PA (CENZ) CENTOCOR INC.
XX
PI Heavner GA, Knight DM, Scallon BJ, Ghrayeb J;
XX
DR WPI; 2003-804237/75.
XX
PT New CDR mimetibody comprising a portion of a heavy or light chain
PT variable region comprising human framework or ligand binding region,
PT useful for preparing a composition for treating e.g., immune,
PT cardiovascular or neurologic disease.
XX
PS Example 2; SEQ ID NO 991; 97pp; English.
XX
CC This invention relates to novel mammalian CDR mimetibodies, specific
CC portions or variants thereof. Specifically, it refers to an antibody
CC fragment where a protein has been inserted into, or replaces a portion
CC of, one or more CDR regions, such that each CDR mimetibody comprises at
CC least one portion of a heavy chain or light chain variable region, which
CC itself comprises at least one human framework region and at least one
CC ligand binding region (LBR). The present invention describes human

```
CC   mimetibodies, including modified immunoglobulins and cleavage products
CC   that can be useful in gene therapy and the generation of transgenic
CC   plants and animals. Furthermore, the CDR mimetibody is useful for
CC   preparing compositions for modulating, treating or reducing the symptoms
CC   of immune, cardiovascular, infectious, malignant and/ or neurologic
CC   diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
CC   cardiant, antimicrobial, cytostatic and neuroprotective activities. This
CC   polypeptide sequence is an erythropoietin heavy chain mimetibody of the
CC   invention.
XX
SQ   Sequence 133 AA;

  Query Match             94.1%;  Score 572;  DB 7;  Length 133;
  Best Local Similarity   84.2%;  Pred. No. 6e-45;
  Matches  112;  Conservative    0;  Mismatches    3;  Indels   18;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAG-------------- 105
              ||||| |||||||||||||||||||||||||||||||||||||| |
Db         61 ADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISGGGGTYSCHTGPLTWVC 120

Qy        106 ---GNYYYYGMDV 115
                  | ||||||||
Db        121 KPQGGYYYYGMDV 133


RESULT 5
AAM51169
ID   AAM51169 standard; protein; 146 AA.
XX
AC   AAM51169;
XX
DT   10-JUN-2002  (first entry)
XX
DE   Human recombinant mAb TNV15 heavy chain variable region.
XX
KW   Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;
KW   complementarity determining region; antirheumatic; antiarthritic;
KW   antiulcer; antiasthmatic; antiallergic; antiinflammatory; antisickling;
KW   antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;
KW   antianginal; cardiant; antibacterial; virucide; fungicide; antileprotic;
KW   protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;
KW   human; diagnosis; therapy; TNV15; monoclonal antibody; mAb.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /label= Signal_peptide
FT                   /note= "amino acids 1-7 are PCR primer-encoded and may
FT                   differ from the native sequence"
FT   Protein         20. .146
FT                   /label= Mature_protein
FT   Region          31. .49
FT                   /label= FR1
FT   Region          50. .54
FT                   /label= CDR1
FT   Region          55. .68
FT                   /label= FR2
FT   Region          69. .85
FT                   /label= CDR2
FT   Region          86. .117
FT                   /label= FR3
FT   Region          118. .135
FT                   /label= CDR3
FT   Misc-difference 126
FT                   /note= "encoded by A"
FT   Region          136. .146
FT                   /label= J6
XX

PN   WO200212502-A2.
XX
PD   14-FEB-2002.
XX
PF   07-AUG-2001; 2001WO-US024785.
XX
PR   07-AUG-2000; 2000US-0223360P.
PR   29-SEP-2000; 2000US-0236826P.
PR   01-AUG-2001; 2001US-00920137.
XX
PA   (CENZ ) CENTOCOR INC.
XX
PI   Giles-Komar J,  Knight DM,  Heavner G,  Scallon B,  Shealy D;
XX
DR   WPI; 2002-217194/27.
DR   N-PSDB; ABL53509.
XX
PT   Novel isolated mammalian anti-tumor necrosis factor antibody, useful for
PT   treating sickle cell anemia, diabetes, atherosclerosis, restenosis,
PT   angina pectoris, myocardial infarction, leprosy.
XX
PS   Example 3; Fig 4; 131pp; English.
XX
CC   The present sequence is that of the heavy chain variable region of anti-
CC   tumour necrosis factor (TNF) human recombinant monoclonal antibody (mAb)
CC   TNV15. TNV15 was 1 of 8 human mAbs produced from a GenTNV fusion using
CC   spleen cells from a hybrid mouse containing human variable and constant
CC   region antibody transgenes that was immunised with human TNF alpha. The
CC   human mAbs bound immobilised human TNF alpha with high avidity and had a
CC   totally human IgG1, kappa isotype. They showed relatedness to each other
CC   and to the human germline DP-46 heavy chain sequence (see AAM51167). The
CC   invention provides isolated human, primate, rodent, mammalian, chimeric,
CC   humanised and/or complementarity determining region (CDR)-grafted anti-
CC   TNF antibodies, immunoglobulins, cleavage products and other specified
CC   portions and variants, as well as anti-TNF antibody compositions,
CC   encoding or complementary nucleic acids, vectors, host cells,
CC   compositions, formulations, devices, transgenic animals, transgenic
CC   plants, and methods of making and using them. The anti-TNF antibody
CC   comprises at least a portion of an immunoglobulin molecule, especially
CC   the heavy chain and/or light chain variable regions given in the present
CC   sequence and in AAM51165, or either all of the CDRs of the heavy chain
CC   (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-
CC   63). The antibodies may inhibit TNF-induced cell adhesion molecules,
CC   inhibit TNF binding to receptor, or provide Arthritic Index improvement
CC   in a mouse model. They are useful for diagnosing or treating a TNF
CC   related condition in a cell, tissue, organ or animal (claimed) such as
CC   rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's
CC   pathology, sickle cell anaemia, diabetes, a cardiovascular disease such
CC   as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or
CC   myocardial infarction, an infectious disease in a cell such as bacterial,
CC   viral, and fungal infections, pneumonia, leprosy and malaria, a malignant
CC   disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
CC   lymphoma and multiple myeloma, or a neurological disease such as multiple
CC   sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and
CC   Creutzfeldt-Jakob disease
XX
SQ   Sequence 146 AA;

  Query Match             94.0%;  Score 571.5;  DB 5;  Length 146;
  Best Local Similarity   94.8%;  Pred. No. 7.4e-45;
  Matches  110;  Conservative    1;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||||||||||||||||||||||||||||||||||| | |||||| |
Db         20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAFILYDGSNKKY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGN-YYYYGMDV 115
              |||||||||||||||| ||||||||||||||||||||||:||||| ||||||||
Db         80 ADSVKGRFTISRDNSKNALYLQMNSLRAEDTAVYYCARDRGVSAGGNYYYYYGMDV 135


RESULT 6
AAM51168
```

```
ID   AAM51168 standard; protein; 146 AA.
XX
AC   AAM51168;
XX
DT   10-JUN-2002  (first entry)
XX
DE   Human recombinant mAb TNV14 heavy chain variable region.
XX
KW   Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;
KW   complementarity determining region; antirheumatic; antiarthritic;
KW   antiulcer; antiasthmatic; antiallergic; antiinflammatory; antisickling;
KW   antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;
KW   antianginal; cardiant; antibacterial; virucide; fungicide; antileprotic;
KW   protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;
KW   human; diagnosis; therapy; TNV14; monoclonal antibody; mAb.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /label= Signal_peptide
FT                   /note= "amino acids 1-7 are PCR primer-encoded and may
FT                   differ from the native sequence"
FT   Protein         20. .146
FT                   /label= Mature_protein
FT   Region          31. .49
FT                   /label= FR1
FT   Region          50. .54
FT                   /label= CDR1
FT   Region          55. .68
FT                   /label= FR2
FT   Region          69. .85
FT                   /label= CDR2
FT   Region          86. .117
FT                   /label= FR3
FT   Region          118. .135
FT                   /label= CDR3
FT   Misc-difference 126
FT                   /note= "encoded by A"
FT   Region          136. .146
FT                   /label= J6
XX
PN   WO200212502-A2.
XX
PD   14-FEB-2002.
XX
PF   07-AUG-2001; 2001WO-US024785.
XX
PR   07-AUG-2000; 2000US-0223360P.
PR   29-SEP-2000; 2000US-0236826P.
PR   01-AUG-2001; 2001US-00920137.
XX
PA   (CENZ ) CENTOCOR INC.
XX
PI   Giles-Komar J,  Knight DM,  Heavner G,  Scallon B,  Shealy D;
XX
DR   WPI; 2002-217194/27.
DR   N-PSDB; ABL53508.
XX
PT   Novel isolated mammalian anti-tumor necrosis factor antibody, useful for
PT   treating sickle cell anemia, diabetes, atherosclerosis, restenosis,
PT   angina pectoris, myocardial infarction, leprosy.
XX
PS   Example 3; Fig 4; 131pp; English.
XX
CC   The present sequence is that of the heavy chain variable region of anti-
CC   tumour necrosis factor (TNF) human recombinant monoclonal antibody (mAb)
CC   TNV14. TNV14 was 1 of 8 human mAbs produced from a GenTNV fusion using
CC   spleen cells from a hybrid mouse containing human variable and constant
CC   region antibody transgenes that was immunised with human TNF alpha. The
CC   human mAbs bound immobilised human TNF alpha with high avidity and had a
CC   totally human IgG1, kappa isotype. They showed relatedness to each other
CC   and to the human germline DP-46 heavy chain sequence (see AAM51167). The
CC   invention provides isolated human, primate, rodent, mammalian, chimeric,
CC   humanised and/or complementarity determining region (CDR)-grafted anti-
CC   TNF antibodies, immunoglobulins, cleavage products and other specified
CC   portions and variants, as well as anti-TNF antibody compositions,
CC   encoding or complementary nucleic acids, vectors, host cells,
CC   compositions, formulations, devices, transgenic animals, transgenic
CC   plants, and methods of making and using them. The anti-TNF antibody
CC   comprises at least a portion of an immunoglobulin molecule, especially
CC   the heavy chain and/or light chain variable regions given in the present
CC   sequence and in AAM51165, or either all of the CDRs of the heavy chain
CC   (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-
CC   63). The antibodies may inhibit TNF-induced cell adhesion molecules,
CC   inhibit TNF binding to receptor, or provide Arthritic Index improvement
CC   in a mouse model. They are useful for diagnosing or treating a TNF
CC   related condition in a cell, tissue, organ or animal (claimed) such as
CC   rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's
CC   pathology, sickle cell anaemia, diabetes, a cardiovascular disease such
CC   as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or
CC   myocardial infarction, an infectious disease in a cell such as bacterial,
CC   viral, and fungal infections, pneumonia, leprosy and malaria, a malignant
CC   disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
CC   lymphoma and multiple myeloma, or a neurological disease such as multiple
CC   sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and
CC   Creutzfeldt-Jakob disease
XX
SQ   Sequence 146 AA;

  Query Match           93.7%;  Score 569.5;  DB 5;  Length 146;
  Best Local Similarity  94.8%;  Pred. No. 1.1e-44;
  Matches  110;  Conservative    2;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||:| ||||:| |
Db         20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAIILYDGSSKKY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGN-YYYYGMDV 115
              ||||| |||||||||||||||||||||||||||||||||||||||| |||||||
Db         80 ADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYYGMDV 135


RESULT 7
AAM51171
ID   AAM51171 standard; protein; 146 AA.
XX
AC   AAM51171;
XX
DT   10-JUN-2002  (first entry)
XX
DE   Human recombinant mAb TNV148(B) heavy chain variable region.
XX
KW   Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;
KW   complementarity determining region; antirheumatic; antiarthritic;
KW   antiulcer; antiasthmatic; antiallergic; antiinflammatory; antisickling;
KW   antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;
KW   antianginal; cardiant; antibacterial; virucide; fungicide; antileprotic;
KW   protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;
KW   human; diagnosis; therapy; TNV148; monoclonal antibody; mAb.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /label= Signal_peptide
FT                   /note= "amino acids 1-7 are PCR primer-encoded and may
FT                   differ from the native sequence"
FT   Protein         20. .146
FT                   /label= Mature_protein
FT   Region          31. .49
FT                   /label= FR1
FT   Region          50. .54
FT                   /label= CDR1
FT   Region          55. .68
```

```
FT                   /label= FR2
FT   Region          69. .85
FT                   /label= CDR2
FT   Region          86. .117
FT                   /label= FR3
FT   Misc-difference 94
FT                   /note= "wild-type Pro substituted by Ser"
FT   Region          118. .135
FT                   /label= CDR3
FT   Misc-difference 126
FT                   /note= "encoded by A"
FT   Region          136. .146
FT                   /label= J6
XX
PN   WO200212502-A2.
XX
PD   14-FEB-2002.
XX
PF   07-AUG-2001; 2001WO-US024785.
XX
PR   07-AUG-2000; 2000US-0223360P.
PR   29-SEP-2000; 2000US-0236826P.
PR   01-AUG-2001; 2001US-00920137.
XX
PA   (CENZ ) CENTOCOR INC.
XX
PI   Giles-Komar J,  Knight DM,  Heavner G,  Scallon B,  Shealy D;
XX
DR   WPI; 2002-217194/27.
DR   N-PSDB; ABL53511.
XX
PT   Novel isolated mammalian anti-tumor necrosis factor antibody, useful for
PT   treating sickle cell anemia, diabetes, atherosclerosis, restenosis,
PT   angina pectoris, myocardial infarction, leprosy.
XX
PS   Example 3; Fig 4; 131pp; English.
XX
CC   The present sequence is that of the heavy chain variable region of anti-
CC   tumour necrosis factor (TNF) human recombinant monoclonal antibody (mAb)
CC   TNV148(B). TNV148(B) was produced by site-directed mutagenesis of TNV148
CC   (see AAM51170), replacing residue Pro-94 with a germline Ser. TNV148 was
CC   1 of 8 human mAbs produced from a GenTNV fusion using spleen cells from a
CC   hybrid mouse containing human variable and constant region antibody
CC   transgenes that was immunised with human TNF alpha. The human mAbs bound
CC   immobilised human TNF alpha with high avidity and had a totally human
CC   IgG1, kappa isotype. They showed relatedness to each other and to the
CC   human germline DP-46 heavy chain sequence (see AAM51167). The invention
CC   provides isolated human, primate, rodent, mammalian, chimeric, humanised
CC   and/or complementarity determining region (CDR)-grafted anti-TNF
CC   antibodies, immunoglobulins, cleavage products and other specified
CC   portions and variants, as well as anti-TNF antibody compositions,
CC   encoding or complementary nucleic acids, vectors, host cells,
CC   compositions, formulations, devices, transgenic animals, transgenic
CC   plants, and methods of making and using them. The anti-TNF antibody
CC   comprises at least a portion of an immunoglobulin molecule, especially
CC   the heavy chain and/or light chain variable regions given in the present
CC   sequence and in AAM51165, or either all of the CDRs of the heavy chain
CC   (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-
CC   63). The antibodies may inhibit TNF-induced cell adhesion molecules,
CC   inhibit TNF binding to receptor, or provide Arthritic Index improvement
CC   in a mouse model. They are useful for diagnosing or treating a TNF
CC   related condition in a cell, tissue, organ or animal (claimed) such as
CC   rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's
CC   pathology, sickle cell anaemia, diabetes, a cardiovascular disease such
CC   as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or
CC   myocardial infarction, an infectious disease in a cell such as bacterial,
CC   viral, and fungal infections, pneumonia, leprosy and malaria, a malignant
CC   disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
CC   lymphoma and multiple myeloma, or a neurological disease such as multiple
CC   sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and
CC   Creutzfeldt-Jakob disease. TNV148(B) may be especially useful as an
CC   antiinflammatory
XX
SQ   Sequence 146 AA;

  Query Match             93.2%;  Score 566.5;  DB 5;  Length 146;
  Best Local Similarity   94.0%;  Pred. No. 2.1e-44;
  Matches  109;  Conservative    2;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||||||||||||||| |||||||||||||| |||||| :||||||| |
Db         20 QVQLVESGGGVVQPGRSLRLSCAASGFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGN-YYYYGMDV 115
              |||||||||||||||||||||||||||||||||||||||||:|||| ||||||||
Db         80 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGIAAGGNYYYYYGMDV 135


RESULT 8
AAM51170
ID   AAM51170 standard; protein; 146 AA.
XX
AC   AAM51170;
XX
DT   10-JUN-2002  (first entry)
XX
DE   Human recombinant mAb TNV148 heavy chain variable region.
XX
KW   Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;
KW   complementarity determining region; antirheumatic; antiarthritic;
KW   antiulcer; antiasthmatic; antiallergic; antiinflammatory; antisickling;
KW   antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;
KW   antianginal; cardiant; antibacterial; virucide; fungicide; antileprotic;
KW   protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;
KW   human; diagnosis; therapy; TNV148; monoclonal antibody; mAb.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /label= Signal_peptide
FT                   /note= "amino acids 1-7 are PCR primer-encoded and may
FT                   differ from the native sequence"
FT   Protein         20. .146
FT                   /label= Mature_protein
FT   Region          31. .49
FT                   /label= FR1
FT   Region          50. .54
FT                   /label= CDR1
FT   Region          55. .68
FT                   /label= FR2
FT   Region          69. .85
FT                   /label= CDR2
FT   Region          86. .117
FT                   /label= FR3
FT   Region          118. .135
FT                   /label= CDR3
FT   Misc-difference 126
FT                   /note= "encoded by A"
FT   Region          136. .146
FT                   /label= J6
XX
PN   WO200212502-A2.
XX
PD   14-FEB-2002.
XX
PF   07-AUG-2001; 2001WO-US024785.
XX
PR   07-AUG-2000; 2000US-0223360P.
PR   29-SEP-2000; 2000US-0236826P.
PR   01-AUG-2001; 2001US-00920137.
XX
PA   (CENZ ) CENTOCOR INC.
XX
PI   Giles-Komar J,  Knight DM,  Heavner G,  Scallon B,  Shealy D;
XX
```

DR WPI; 2002-217194/27.
DR N-PSDB; ABL53510.
XX
PT Novel isolated mammalian anti-tumor necrosis factor antibody, useful for
PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,
PT angina pectoris, myocardial infarction, leprosy.
XX
PS Example 3; Fig 4; 131pp; English.
XX
CC The present sequence is that of the heavy chain variable region of anti-
CC tumour necrosis factor (TNF) human recombinant monoclonal antibody (mAb)
CC TNV148. TNV148 was 1 of 8 human mAbs produced from a GenTNV fusion using
CC spleen cells from a hybrid mouse containing human variable and constant
CC region antibody transgenes that was immunised with human TNF alpha. The
CC human mAbs bound immobilised human TNF alpha with high avidity and had a
CC totally human IgG1, kappa isotype. They showed relatedness to each other
CC and to the human germline DP-46 heavy chain sequence (see AAM51167). The
CC invention provides isolated human, primate, rodent, mammalian, chimeric,
CC humanised and/or complementarity determining region (CDR)-grafted anti-
CC TNF antibodies, immunoglobulins, cleavage products and other specified
CC portions and variants, as well as anti-TNF antibody compositions,
CC encoding or complementary nucleic acids, vectors, host cells,
CC compositions, formulations, devices, transgenic animals, transgenic
CC plants, and methods of making and using them. The anti-TNF antibody
CC comprises at least a portion of an immunoglobulin molecule, especially
CC the heavy chain and/or light chain variable regions given in the present
CC sequence and in AAM51165, or either all of the CDRs of the heavy chain
CC (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-
CC 63). The antibodies may inhibit TNF-induced cell adhesion molecules,
CC inhibit TNF binding to receptor, or provide Arthritic Index improvement
CC in a mouse model. They are useful for diagnosing or treating a TNF
CC related condition in a cell, tissue, organ or animal (claimed) such as
CC rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's
CC pathology, sickle cell anaemia, diabetes, a cardiovascular disease such
CC as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or
CC myocardial infarction, an infectious disease in a cell such as bacterial,
CC viral, and fungal infections, pneumonia, leprosy and malaria, a malignant
CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
CC lymphoma and multiple myeloma, or a neurological disease such as multiple
CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and
CC Creutzfeldt-Jakob disease. TNV148 may be especially useful as an
CC antiinflammatory
XX
SQ Sequence 146 AA;

Query Match 92.4%; Score 561.5; DB 5; Length 146;
Best Local Similarity 93.1%; Pred. No. 6.2e-44;
Matches 108; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

```
Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||||||||||||||| |||||||||||||| |||||| :||||||| |
Db         20 QVQLVESGGGVVQPGRSLRLSCAASGFIFSSYAMHWVRQAPGNGLEWVAFMSYDGSNKKY 79

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGN-YYYYGMDV 115
              ||||||||||||| |||||||||||||||||||||||||:|||| ||||||||
Db         80 ADSVKGRFTISRDNPKNTLYLQMNSLRAEDTAVYYCARDRGIAAGGNYYYYYGMDV 135
```

RESULT 9
AAM51172
ID AAM51172 standard; protein; 146 AA.
XX
AC AAM51172;
XX
DT 10-JUN-2002 (first entry)
XX
DE Human recombinant mAb TNV196 heavy chain variable region.
XX
KW Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;
KW complementarity determining region; antirheumatic; antiarthritic;
KW antiulcer; antiasthmatic; antiallergic; antiinflammatory; antisickling;
KW antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;
KW antianginal; cardiant; antibacterial; virucide; fungicide; antileprotic;
KW protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;
KW human; diagnosis; therapy; TNV196; monoclonal antibody; mAb.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1. .19
FT		/label= Signal_peptide
FT		/note= "amino acids 1-7 are PCR primer-encoded and may
FT		differ from the native sequence"
FT	Protein	20. .146
FT		/label= Mature_protein
FT	Region	31. .49
FT		/label= FR1
FT	Region	50. .54
FT		/label= CDR1
FT	Region	55. .68
FT		/label= FR2
FT	Region	69. .85
FT		/label= CDR2
FT	Region	86. .117
FT		/label= FR3
FT	Region	118. .135
FT		/label= CDR3
FT	Misc-difference	126
FT		/note= "encoded by A"
FT	Region	136. .146
FT		/label= J6

XX
PN WO200212502-A2.
XX
PD 14-FEB-2002.
XX
PF 07-AUG-2001; 2001WO-US024785.
XX
PR 07-AUG-2000; 2000US-0223360P.
PR 29-SEP-2000; 2000US-0236826P.
PR 01-AUG-2001; 2001US-00920137.
XX
PA (CENZ) CENTOCOR INC.
XX
PI Giles-Komar J, Knight DM, Heavner G, Scallon B, Shealy D;
XX
DR WPI; 2002-217194/27.
DR N-PSDB; ABL53512.
XX
PT Novel isolated mammalian anti-tumor necrosis factor antibody, useful for
PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,
PT angina pectoris, myocardial infarction, leprosy.
XX
PS Example 3; Fig 4; 131pp; English.
XX
CC The present sequence is that of the heavy chain variable region of anti-
CC tumour necrosis factor (TNF) human recombinant monoclonal antibody (mAb)
CC TNV196. TNV196 was 1 of 8 human mAbs produced from a GenTNV fusion using
CC spleen cells from a hybrid mouse containing human variable and constant
CC region antibody transgenes that was immunised with human TNF alpha. The
CC human mAbs bound immobilised human TNF alpha with high avidity and had a
CC totally human IgG1, kappa isotype. They showed relatedness to each other
CC and to the human germline DP-46 heavy chain sequence (see AAM51167). The
CC invention provides isolated human, primate, rodent, mammalian, chimeric,
CC humanised and/or complementarity determining region (CDR)-grafted anti-
CC TNF antibodies, immunoglobulins, cleavage products and other specified
CC portions and variants, as well as anti-TNF antibody compositions,
CC encoding or complementary nucleic acids, vectors, host cells,
CC compositions, formulations, devices, transgenic animals, transgenic
CC plants, and methods of making and using them. The anti-TNF antibody
CC comprises at least a portion of an immunoglobulin molecule, especially
CC the heavy chain and/or light chain variable regions given in the present
CC sequence and in AAM51165, or either all of the CDRs of the heavy chain
CC (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-
CC 63). The antibodies may inhibit TNF-induced cell adhesion molecules,
CC inhibit TNF binding to receptor, or provide Arthritic Index improvement

CC in a mouse model. They are useful for diagnosing or treating a TNF
CC related condition in a cell, tissue, organ or animal (claimed) such as
CC rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's
CC pathology, sickle cell anaemia, diabetes, a cardiovascular disease such
CC as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or
CC myocardial infarction, an infectious disease in a cell such as bacterial,
CC viral, and fungal infections, pneumonia, leprosy and malaria, a malignant
CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
CC lymphoma and multiple myeloma, or a neurological disease such as multiple
CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and
CC Creutzfeldt-Jakob disease
XX
SQ Sequence 146 AA;

Query Match 92.4%; Score 561.5; DB 5; Length 146;
Best Local Similarity 93.1%; Pred. No. 6.2e-44;
Matches 108; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
Db 20 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAFISYDGSNKKS 79

Qy 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGN-YYYYGMDV 115
Db 80 ADSVKGRFTVSRDNSKNTLFLQMNSLRAEDTAVFYCARDRGIGAGGNYYYYYGMDV 135

RESULT 10
ADA89238
ID ADA89238 standard; protein; 124 AA.
XX
AC ADA89238;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human antibody T3F2 heavy chain amino acid sequence SEQ ID NO:82.
XX
KW immunoglobulin; Ig; heavy chain variable domain;
KW light chain variable domain; major histocompatibility complex; MHC;
KW gp100; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;
KW cancer.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003070752-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005128.
XX
PR 20-FEB-2002; 2002US-0358994P.
XX
PA (DYAX-) DYAX CORP.
PA (TECR) TECHNION RES & DEV FOUND LTD.
XX
PI Hoogenboom HRJM, Reiter Y;
XX
DR WPI; 2003-663847/62.
DR N-PSDB; ADA89237.
XX
PT New protein comprising an immunoglobulin heavy chain variable (VH) domain
PT and an immunoglobulin light chain variable (VL) domain, useful for
PT preparing a composition for treating or preventing a cancerous disorder.
XX
PS Disclosure; Fig 19B; 224pp; English.
XX
CC The present invention describes a protein comprising an immunoglobulin
CC (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL)
CC domain. The protein binds a complex comprising a major histocompatibility
CC complex (MHC) and a peptide, does not substantially bind the MHC in the
CC absence of the bound peptide, and does not substantially bind the peptide
CC in the absence of the MHC. The peptide is a peptide fragment of gp100,
CC MUC1, TAX or hTERT. ALso described: (1) a pharmaceutical composition
CC comprising the novel protein and a carrier; (2) a cytotoxic T cell
CC comprising one or more nucleic acids for expressing the Ig that binds a
CC complex having an MHC and a peptide, does not substantially bind the MHC
CC in the absence of the bound peptide, and does not substantially bind the
CC peptide in the absence of the MHC; (3) an isolated nucleic acid
CC comprising a first segment that encodes the Ig variable domain; (4) a
CC host cell comprising heterologous nucleic acid sequences that encodes the
CC novel protein; (5) a transgenic animal whose genome includes heterologous
CC nucleic acid sequences that encode the protein; (6) identifying the
CC protein that specifically binds the MHC-peptide complex; (7) expressing
CC an antigen-binding protein; (8) ablating or killing a target cell that
CC displays a peptide on a surface MHC molecule; (9) treating or preventing
CC a cancerous disorder in a subject; and (10) detecting an MHC-peptide
CC complex in a sample. A protein of the invention has cytostatic activity,
CC and can be used in gene therapy. The protein is useful for preparing a
CC composition for treating or preventing a cancerous disorder. The present
CC sequence represents the heavy chain of an antibody which binds to an MHC-
CC peptide complex where the peptide component in as peptide fragment of
CC TAX.
XX
SQ Sequence 124 AA;

Query Match 91.0%; Score 553; DB 6; Length 124;
Best Local Similarity 92.2%; Pred. No. 3.1e-43;
Matches 106; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

Qy 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
Db 1 QVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
Db 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARD--FDYGDSYYYYGMDV 113

RESULT 11
AAY17954
ID AAY17954 standard; protein; 127 AA.
XX
AC AAY17954;
XX
DT 04-AUG-1999 (first entry)
XX
DE Human D4.5 heavy chain variable region.
XX
KW Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
KW autoimmune disease; scFv-antibody; single-chain Fv.
XX
OS Homo sapiens.
XX
PN WO9925818-A1.
XX
PD 27-MAY-1999.
XX
PF 16-NOV-1998; 98WO-EP007313.
XX
PR 17-NOV-1997; 97EP-00120096.
XX
PA (KUFE/) KUFER P.
XX
PI Kufer P, Raum T, Borschert K, Zettl F, Lutterbuese R;
XX
DR WPI; 1999-338004/28.
DR N-PSDB; AAX77236.
XX
PT Phage display system for identification of binding site domains retaining
PT capacity to bind an epitope.
XX
PS Disclosure; Fig 3.1; 152pp; English.
XX
CC The invention relates to a method of identifying binding site domains
CC (BSD) that retain the capacity of binding to a predetermined epitope when

CC positioned C-terminal of at least one further domain in a recombinant bi-
CC or multivalent polypeptide. The method comprises (a) testing a panel of
CC BSD displayed on the surface of a biological display system as part of a
CC fusion protein for binding to a predetermined epitope, where the fusion
CC protein comprises an additional domain positioned N-terminal of the BSD
CC and an amino acid sequence that mediates anchoring of the fusion protein
CC to the surface of the display system; and (b) identifying a BSD that
CC binds to the predetermined epitope. The method is useful to identify bi-
CC or multivalent polypeptides that comprise antibody binding sites capable
CC of efficiently binding to the corresponding antigen. The polypeptides or
CC antibodies identified by the method are useful therapeutically and
CC diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody
CC fragments that bind independently of their position within bifunctional
CC single-chain fusion proteins can be isolated from combinatorial antibody
CC libraries using the new in vitro method
XX
SQ Sequence 127 AA;

Query Match 90.5%; Score 550.5; DB 2; Length 127;
Best Local Similarity 90.5%; Pred. No. 5.4e-43;
Matches 105; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

```
Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||:|||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGN-YYYYGMDV 115
              ||||||||||||||||||||||||||||||||||:| |  :|   ||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDMGWGSGWRPYYYYGMDV 116
```

RESULT 12
AAW80815
ID AAW80815 standard; protein; 138 AA.
XX
AC AAW80815;
XX
DT 16-FEB-1999 (first entry)
XX
DE Amino acid sequence of human D4.5 heavy chain variable region.
XX
KW Human; D4.5 heavy chain variable region; receptor; antigen; tumour;
KW auto-immune disease; graft rejection; allergy; inflammatory disease;
KW endocrine disease; degenerative disease.
XX
OS Homo sapiens.
XX
PN WO9846645-A2.
XX
PD 22-OCT-1998.
XX
PF 14-APR-1998; 98WO-EP002180.
XX
PR 14-APR-1997; 97EP-00106109.
XX
PA (KUFE/) KUFER P.
PA (RAUM/) RAUM T.
XX
PI Kufer P, Raum T;
XX
DR WPI; 1998-594564/50.
DR N-PSDB; AAV68537.
XX
PT Production of anti-human antigen receptors - by selecting a combination
PT of functionally rearranged VH and VL immunoglobulin chains expressed from
PT a recombinant vector.
XX
PS Claim 9; Fig 7; 84pp; English.
XX
CC This is the amino acid sequence of the human D4.5 heavy chain variable
CC region, used in the method of the invention. for providing receptors that
CC can be used for targeting antigens in humans without being immunogenic
CC themselves. Such receptors can be used for treating diseases such as
CC tumours or auto-immune diseases, graft rejection after transplantation,
CC infectious diseases by targeting cellular receptors as well as allergic,
CC inflammatory, endocrine and degenerative diseases by targeting key
CC molecules involved in the pathological process
XX
SQ Sequence 138 AA;

Query Match 90.5%; Score 550.5; DB 2; Length 138;
Best Local Similarity 90.5%; Pred. No. 6e-43;
Matches 105; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

```
Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||:|||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db          1 EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGN-YYYYGMDV 115
              ||||||||||||||||||||||||||||||||||:| |  :|   ||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDMGWGSGWRPYYYYGMDV 116
```

RESULT 13
ABP45720
ID ABP45720 standard; protein; 252 AA.
XX
AC ABP45720;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLyS binding scFv SEQ ID 1731.
XX
KW BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
DR WPI; 2002-114799/15.
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 2468-2469; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC and so may be used to detect and quantitate the presence of BLyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLyS. They may also be

CC administered to treat diseases associated with aberrant BLyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 252 AA;

Query Match 90.5%; Score 550.5; DB 5; Length 252;
Best Local Similarity 91.6%; Pred. No. 1.2e-42;
Matches 109; Conservative 0; Mismatches 5; Indels 5; Gaps 2;

Qy 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
Db 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR----GISAGGNYYYYGMDV 115
Db 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRLEYYDILT-GYYYYYGMDV 118

RESULT 14
ADG96547
ID ADG96547 standard; protein; 252 AA.
XX
AC ADG96547;
XX
DT 11-MAR-2004 (first entry)
XX
DE Single chain antibody that immunospecifically binds BLyS SeqID 1731.
XX
KW antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;
KW B cell proliferation; differentiation; scFv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS Unidentified.
XX
PN WO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PF 14-NOV-2002; 2002WO-US036496.
XX
PR 16-NOV-2001; 2001US-0331469P.
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
DR WPI; 2003-505530/47.
XX
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (BLys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
PS Example 1; SEQ ID NO 1731; 394pp; English.
XX
CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey BLyS. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of BLyS or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiarthritic, neuroprotective,
CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds BLyS of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directely from WIPO at ftp.wipo.int/pub/published pct_sequences.
XX
SQ Sequence 252 AA;

Query Match 90.5%; Score 550.5; DB 7; Length 252;
Best Local Similarity 91.6%; Pred. No. 1.2e-42;
Matches 109; Conservative 0; Mismatches 5; Indels 5; Gaps 2;

Qy 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
Db 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR----GISAGGNYYYYGMDV 115
Db 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRLEYYDILT-GYYYYYGMDV 118

RESULT 15
AAY44994
ID AAY44994 standard; protein; 523 AA.
XX
AC AAY44994;
XX
DT 23-MAY-2000 (first entry)
XX
DE HD70scFv-CH1-GM-CSF chain.
XX
KW HD70; single-chain variable fragment; scFv; 17-1A antigen; human; EpCAM;
KW epithelial cell adhesion molecule; inflammatory cytokine; GM-CSF;
KW granulocyte/macrophage colony stimulating factor; heterominibody;
KW CH1-domain; multifunctional compound; heavy chain constant domain;
KW immunoglobulin; cytostatic; immunostimulatory; antileukaemia; diagnosis;
KW antiproliferative; prevention; treatment; malignant; haematopoietic cell;
KW lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma.
XX
OS Homo sapiens.
XX
PN WO200006605-A2.
XX
PD 10-FEB-2000.
XX
PF 28-JUL-1999; 99WO-EP005416.
XX
PR 28-JUL-1998; 98EP-00114082.
XX
PA (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
XX
PI Kufer P, Dreier T, Baeuerle PA, Borschert K, Zettl F;
XX
DR WPI; 2000-195265/17.
DR N-PSDB; AAZ50587.
XX
PT New multifunctional compounds useful for preventing and/or treating
PT malignant cell growth and for detection and diagnosis.
XX
PS Example 10; Fig 55A; 166pp; English.
XX
CC The patent discloses heterominibodies which are multifunctional compounds
CC produceable in a mammalian host cell as a secretable and fully functional
CC heterodimer of two polypeptide chains, where one of the polypeptide
CC chains comprises, a CH1-domain (constant domain of an immunoglobulin
CC heavy chain) and the other chain comprises CL-domain (constant domain of
CC an immunoglobulin light chain). The polypeptide chains further comprise,

CC fused to the constant domains at least two (poly)peptides having
CC different receptor or ligand functions, where further at least two of the
CC different (poly)peptides lack an intrinsic affinity for one another and
CC are linked via the constant domains. The heterominibodies have
CC cytostatic, immunostimulatory, antileukaemia and antiproliferative
CC activities. These compounds can be used for diagnosing, preventing and
CC treating malignant cell growth related to malignancies of haematopoietic
CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
CC melanomas and sarcomas. The present sequence is the left chain of a
CC heterominibody comprising HD70 single-chain Fv (scFv) fragment N-
CC terminally linked to human CH1 domain which bears at its C-terminus the
CC human inflammatory cytokine granulocyte/macrophage colony stimulating
CC factor (GM-CSF), plus a hexahistidine sequence for ease of purification.
CC HD70 scFv specifically recognises the human epithelial cell adhesion
CC molecule (EpCAM) also called 17-1A antigen
XX
SQ Sequence 523 AA;

Query Match 90.5%; Score 550.5; DB 3; Length 523;
Best Local Similarity 90.5%; Pred. No. 2.6e-42;
Matches 105; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

```
Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||:||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        142 EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 201

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGN-YYYYGMDV 115
              |||||||||||||||||||||||||||||||||||:| |  :|   ||||||||
Db        202 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDMGWGSGWRPYYYYGMDV 257
```

RESULT 16
AAY44995
ID AAY44995 standard; protein; 524 AA.
XX
AC AAY44995;
XX
DT 23-MAY-2000 (first entry)
XX
DE HD70scFv-Ck-interleukin 2.
XX
KW HD70; single-chain Fv fragment; scFv; antibody; 17-1A antigen; human;
KW EpCAM; epithelial cell adhesion molecule; inflammatory cytokine; IL-2;
KW interleukin-2; Ck-domain; kappa light chain constant domain;
KW heterominibody; multifunctional compound; immunoglobulin; cytostatic;
KW immunostimulatory; antileukaemia; diagnosis; prevention;
KW antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;
KW leukaemia; solid tumour; carcinoma; melanoma; sarcoma.
XX
OS Homo sapiens.
XX
PN WO200006605-A2.
XX
PD 10-FEB-2000.
XX
PF 28-JUL-1999; 99WO-EP005416.
XX
PR 28-JUL-1998; 98EP-00114082.
XX
PA (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
XX
PI Kufer P, Dreier T, Baeuerle PA, Borschert K, Zettl F;
XX
DR WPI; 2000-195265/17.
DR N-PSDB; AAZ50588.
XX
PT New multifunctional compounds useful for preventing and/or treating
PT malignant cell growth and for detection and diagnosis.
XX
PS Example 10; Fig 55B; 166pp; English.
XX
CC The patent discloses heterominibodies which are multifunctional compounds
CC produceable in a mammalian host cell as a secretable and fully functional
CC heterodimer of two polypeptide chains, where one of the polypeptide
CC chains comprises, a CH1-domain (constant domain of an immunoglobulin
CC heavy chain) and the other chain comprises CL-domain (constant domain of
CC an immunoglobulin light chain). The polypeptide chains further comprise,
CC fused to the constant domains at least two (poly)peptides having
CC different receptor or ligand functions, where further at least two of the
CC different (poly)peptides lack an intrinsic affinity for one another and
CC are linked via the constant domains. The heterominibodies have
CC cytostatic, immunostimulatory, antileukaemia and antiproliferative
CC activities. These compounds can be used for diagnosing, preventing and
CC treating malignant cell growth related to malignancies of haematopoietic
CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
CC melanomas and sarcomas. The present sequence is the right chain of a
CC heterominibody comprising HD70 single-chain Fv (scFv) fragment N-
CC terminally linked to human Ck domain (constant domain of immunoglobulin-
CC kappa light chain) which bears at its C-terminus the human inflammatory
CC cytokine interleukin-2 (IL-2). HD70 scFv specifically recognises the
CC human epithelial cell adhesion molecule (EpCAM) also called 17-1A antigen
XX
SQ Sequence 524 AA;

Query Match 90.5%; Score 550.5; DB 3; Length 524;
Best Local Similarity 90.5%; Pred. No. 2.6e-42;
Matches 105; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

```
Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              :|||:||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        142 EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYY 201

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGN-YYYYGMDV 115
              |||||||||||||||||||||||||||||||||||:| |  :|   ||||||||
Db        202 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDMGWGSGWRPYYYYGMDV 257
```

RESULT 17
ADK18593
ID ADK18593 standard; protein; 126 AA.
XX
AC ADK18593;
XX
DT 06-MAY-2004 (first entry)
XX
DE Anti-human PDGF-D antibody heavy chain protein sequence.
XX
KW antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003057857-A2.
XX
PD 17-JUL-2003.
XX
PF 06-JAN-2003; 2003WO-US000398.
XX
PR 07-JAN-2002; 2002US-00041860.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX
DR WPI; 2003-587119/55.
XX
PT New human monoclonal antibody that binds to platelet-derived growth
PT factor-D (PDGF-D), useful for treating chronic and recurrent human
PT diseases, such as inflammation, autoimmunity and cancer.
XX
PS Disclosure; SEQ ID NO 17; 255pp; English.
XX
CC The invention relates to a human monoclonal antibody that binds to
CC platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC treating chronic and recurrent human diseases, such as inflammation,
CC autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are

```
CC   useful for modulating collagen formation, and for staging various
CC   cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC   generated using an active protein fragment of the gene product from the
CC   clone 30664188.0.99 arising in the conditioned medium obtained when
CC   HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC   sequence corresponds to a protein used in the invention.
XX
SQ   Sequence 126 AA;

  Query Match             90.5%;  Score 550;  DB 7;  Length 126;
  Best Local Similarity   91.3%;  Pred. No. 6e-43;
  Matches  105;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||:|||||||||||||||| |||||||||||||||||| ||||||||
Db          1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||:|    | || |||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGYRYAGYYYDYGMDV 115


RESULT 18
ADK18785
ID   ADK18785 standard; protein; 126 AA.
XX
AC   ADK18785;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Anti-human PDGF-D antibody protein related sequence #11.
XX
KW   antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO2003057857-A2.
XX
PD   17-JUL-2003.
XX
PF   06-JAN-2003; 2003WO-US000398.
XX
PR   07-JAN-2002; 2002US-00041860.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Corvalan JRF,  Jia X,  Feng X,  Yang X,  Chen F,  Gazit G,  Weber R;
PI   Bezabeh B;
XX
DR   WPI; 2003-587119/55.
XX
PT   New human monoclonal antibody that binds to platelet-derived growth
PT   factor-D (PDGF-D), useful for treating chronic and recurrent human
PT   diseases, such as inflammation, autoimmunity and cancer.
XX
PS   Disclosure; SEQ ID NO 209; 255pp; English.
XX
CC   The invention relates to a human monoclonal antibody that binds to
CC   platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC   treating chronic and recurrent human diseases, such as inflammation,
CC   autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC   useful for modulating collagen formation, and for staging various
CC   cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC   generated using an active protein fragment of the gene product from the
CC   clone 30664188.0.99 arising in the conditioned medium obtained when
CC   HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC   sequence corresponds to a protein used in the invention.
XX
SQ   Sequence 126 AA;

  Query Match             90.5%;  Score 550;  DB 7;  Length 126;
  Best Local Similarity   91.3%;  Pred. No. 6e-43;
  Matches  105;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||:|||||||||||||||| |||||||||||||||||| ||||||||
Db          1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||:|    | || |||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGYRYAGYYYDYGMDV 115


RESULT 19
ADK18858
ID   ADK18858 standard; protein; 126 AA.
XX
AC   ADK18858;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Anti-human PDGF-D antibody protein related sequence #84.
XX
KW   antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO2003057857-A2.
XX
PD   17-JUL-2003.
XX
PF   06-JAN-2003; 2003WO-US000398.
XX
PR   07-JAN-2002; 2002US-00041860.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Corvalan JRF,  Jia X,  Feng X,  Yang X,  Chen F,  Gazit G,  Weber R;
PI   Bezabeh B;
XX
DR   WPI; 2003-587119/55.
XX
PT   New human monoclonal antibody that binds to platelet-derived growth
PT   factor-D (PDGF-D), useful for treating chronic and recurrent human
PT   diseases, such as inflammation, autoimmunity and cancer.
XX
PS   Disclosure; SEQ ID NO 282; 255pp; English.
XX
CC   The invention relates to a human monoclonal antibody that binds to
CC   platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC   treating chronic and recurrent human diseases, such as inflammation,
CC   autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC   useful for modulating collagen formation, and for staging various
CC   cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC   generated using an active protein fragment of the gene product from the
CC   clone 30664188.0.99 arising in the conditioned medium obtained when
CC   HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC   sequence corresponds to a protein used in the invention.
XX
SQ   Sequence 126 AA;

  Query Match             90.5%;  Score 550;  DB 7;  Length 126;
  Best Local Similarity   91.3%;  Pred. No. 6e-43;
  Matches  105;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||:|||||||||||||||| |||||||||||||||||| ||||||||
Db          1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||:|    | || |||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGYRYAGYYYDYGMDV 115


RESULT 20
ADL25404
```

ID ADL25404 standard; protein; 126 AA.
XX
AC ADL25404;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human mAb 1.17 heavy chain variable region protein SEQ ID NO:14.
XX
KW antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;
KW nephritis; mesangial cell proliferation inhibition;
KW mesangial proliferative glomerulonephritis; nephrotropic;
KW antiinflammatory; dermatological; immunosuppressive; antidiabetic;
KW gene therapy; human; monoclonal antibody; mAb.
XX
OS Homo sapiens.
XX
PN WO2004024098-A2.
XX
PD 25-MAR-2004.
XX
PF 16-SEP-2003; 2003WO-US029414.
XX
PR 16-SEP-2002; 2002US-0411137P.
XX
PA (ABGE-) ABGENIX INC.
PA (CURA-) CURAGEN CORP.
XX
PI Floege J, Gazit-Bornstein G, Keyt B, Larochelle WJ, Lichenstein H;
XX
DR WPI; 2004-269881/25.
DR N-PSDB; ADL25403.
XX
PT Use of an antibody or its binding fragment that binds platelet derived
PT growth factor-DD (PDGF-DD) for preparing a medicament for treating
PT nephritis.
XX
PS Disclosure; SEQ ID NO 14; 115pp; English.
XX
CC The present invention describes an antibody or its binding fragment that
CC binds platelet derived growth factor-DD (PDGF-DD), where the antibody is
CC useful in preparing a medicament for treating nephritis. Also described:
CC (1) a method of detecting nephritis; (2) a method of treating nephritis;
CC (3) a method of inhibiting mesangial cell proliferation; and (4) a method
CC of treating mesangial proliferative glomerulonephritis. The antibody has
CC nephrotropic, antiinflammatory, dermatological, immunosuppressive and
CC antidiabetic activities, and can be used in gene therapy. The antibody or
CC its binding fragment, that binds PDGF-DD, can be used in preparing a
CC medicament for treating nephritis and related disorders, e.g., mesangial
CC proliferative glomerulonephritis. The present sequence represents a human
CC monoclonal antibody (mAb) variable region sequence, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 126 AA;

Query Match 90.5%; Score 550; DB 8; Length 126;
Best Local Similarity 91.3%; Pred. No. 6e-43;
Matches 105; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

```
Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||||:|||||||||||||||| |||||||||||||||| ||||||||
Db          1 QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              ||||||||||||||||||||||||||||||||||:|    | || |||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDQGYRYAGYYYDYGMDV 115
```

RESULT 21
ADP22222
ID ADP22222 standard; protein; 126 AA.
XX
AC ADP22222;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human anti-TNFa antibody light chain variable region SEQ ID NO:128.
XX
KW human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
KW anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;
KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
KW prostrate cancer; immuno-mediated inflammatory disease;
KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
KW septic shock; cachexia; anorexia; multiple sclerosis.
XX
OS Homo sapiens.
XX
PN WO2004050683-A2.
XX
PD 17-JUN-2004.
XX
PF 02-DEC-2003; 2003WO-US038281.
XX
PR 02-DEC-2002; 2002US-0430729P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Babcook JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;
PI Manchulencho K, Faggioni R, Senaldi G, Qiaojuan JS;
XX
DR WPI; 2004-480601/45.
DR N-PSDB; ADP22221.
XX
PT New recombinant human monoclonal antibody that specifically binds to
PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
PT arthritis.
XX
PS Example 10; SEQ ID NO 128; 213pp; English.
XX
CC The present invention describes a human monoclonal antibody (I) that
CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC (M1) the level of TNFa in a patient sample, comprising contacting with
CC (I), and detecting the level of binding between the antibody and TNFa in
CC the sample; (2) a composition comprising the antibody or its functional
CC fragment and a carrier; (3) treating (M2) an animal suffering from a
CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC animal in need of treatment for the disease by administering the human
CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced
CC apoptosis in an animal by selecting an animal in need of treatment for
CC TNFa induced apoptosis by administering the human monoclonal antibody of
CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
CC disorders, immunomodulator, immunosuppressive, nephrotropic,
CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
CC as a TNFa antagonist. The antibody (I) is useful in the preparation of
CC medicament for treating TNF induced apoptosis, neoplastic disease such as
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer, and prostrate cancer; or immuno-mediated inflammatory
CC diseases such as rheumatoid arthritis, glomerulonephritis,
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC multiple sclerosis. The present sequence represents a human anti-TNFa
CC antibody light chain variable region, which is used in the
CC exemplification of the present invention.

```
XX
SQ   Sequence 126 AA;

  Query Match            89.8%;  Score 546;  DB 8;  Length 126;
  Best Local Similarity   91.3%;  Pred. No. 1.4e-42;
  Matches  105;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||:| |||||||||||||||| ||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||:    || ||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREGIAVAGPPYYYYGMDV 115


RESULT 22
ADP22300
ID   ADP22300 standard; protein; 125 AA.
XX
AC   ADP22300;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human anti-TNFa antibody heavy chain variable region SEQ ID NO:206.
XX
KW   human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
KW   anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;
KW   antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
KW   eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
KW   neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
KW   TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
KW   bladder cancer; lung cancer; glioblastoma; stomach cancer;
KW   endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
KW   prostrate cancer; immuno-mediated inflammatory disease;
KW   rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
KW   restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
KW   septic shock; cachexia; anorexia; multiple sclerosis.
XX
OS   Homo sapiens.
XX
PN   WO2004050683-A2.
XX
PD   17-JUN-2004.
XX
PF   02-DEC-2003; 2003WO-US038281.
XX
PR   02-DEC-2002; 2002US-0430729P.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Babcook JS,  Kang JS,  Foord O,  Green L,  Feng X,  Klakamp S;
PI   Haak-Frendscho M,  Rathanaswami P,  Pigott C,  Liang ML,  Lee R;
PI   Manchulencho K,  Faggioni R,  Senaldi G,  Qiaojuan JS;
XX
DR   WPI; 2004-480601/45.
DR   N-PSDB; ADP22299.
XX
PT   New recombinant human monoclonal antibody that specifically binds to
PT   Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
PT   as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
PT   arthritis.
XX
PS   Example 10; SEQ ID NO 206; 213pp; English.
XX
CC   The present invention describes a human monoclonal antibody (I) that
CC   specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
CC   (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC   two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
CC   and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC   sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC   (M1) the level of TNFa in a patient sample, comprising contacting with
CC   (I), and detecting the level of binding between the antibody and TNFa in
CC   the sample; (2) a composition comprising the antibody or its functional
CC   fragment and a carrier; (3) treating (M2) an animal suffering from a
CC   neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC   animal in need of treatment for the disease by administering the human
CC   monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced
CC   apoptosis in an animal by selecting an animal in need of treatment for
CC   TNFa induced apoptosis by administering the human monoclonal antibody of
CC   (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
CC   antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
CC   disorders, immunomodulator, immunosuppressive, nephrotropic,
CC   neuroprotective, vasotropic and antiapoptotic activities, and can be used
CC   as a TNFa antagonist. The antibody (I) is useful in the preparation of
CC   medicament for treating TNF induced apoptosis, neoplastic disease such as
CC   breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC   stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC   pancreatic cancer, and prostrate cancer; or immuno-mediated inflammatory
CC   diseases such as rheumatoid arthritis, glomerulonephritis,
CC   atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC   disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC   multiple sclerosis. The present sequence represents a human anti-TNFa
CC   antibody heavy chain variable region, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 125 AA;

  Query Match            89.7%;  Score 545.5;  DB 8;  Length 125;
  Best Local Similarity   91.3%;  Pred. No. 1.5e-42;
  Matches  105;  Conservative    3;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              |||||||||||||||||||||||||||||| |||||||||||||||| ||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||:  ::  | ||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARETTVTKEG-YYYYGMDV 114


RESULT 23
ADP22316
ID   ADP22316 standard; protein; 125 AA.
XX
AC   ADP22316;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human anti-TNFa antibody heavy chain variable region SEQ ID NO:222.
XX
KW   human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
KW   anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;
KW   antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
KW   eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
KW   neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
KW   TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
KW   bladder cancer; lung cancer; glioblastoma; stomach cancer;
KW   endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
KW   prostrate cancer; immuno-mediated inflammatory disease;
KW   rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
KW   restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
KW   septic shock; cachexia; anorexia; multiple sclerosis.
XX
OS   Homo sapiens.
XX
PN   WO2004050683-A2.
XX
PD   17-JUN-2004.
XX
PF   02-DEC-2003; 2003WO-US038281.
XX
PR   02-DEC-2002; 2002US-0430729P.
XX
PA   (ABGE-) ABGENIX INC.
XX
```

PI Babcook JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;
PI Manchulencho K, Faggioni R, Senaldi G, Qiaojuan JS;
XX
DR WPI; 2004-480601/45.
DR N-PSDB; ADP22315.
XX
PT New recombinant human monoclonal antibody that specifically binds to
PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
PT arthritis.
XX
PS Example 10; SEQ ID NO 222; 213pp; English.
XX
CC The present invention describes a human monoclonal antibody (I) that
CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC (M1) the level of TNFa in a patient sample, comprising contacting with
CC (I), and detecting the level of binding between the antibody and TNFa in
CC the sample; (2) a composition comprising the antibody or its functional
CC fragment and a carrier; (3) treating (M2) an animal suffering from a
CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC animal in need of treatment for the disease by administering the human
CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced
CC apoptosis in an animal by selecting an animal in need of treatment for
CC TNFa induced apoptosis by administering the human monoclonal antibody of
CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
CC disorders, immunomodulator, immunosuppressive, nephrotropic,
CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
CC as a TNFa antagonist. The antibody (I) is useful in the preparation of
CC medicament for treating TNF induced apoptosis, neoplastic disease such as
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer, and prostrate cancer; or immuno-mediated inflammatory
CC diseases such as rheumatoid arthritis, glomerulonephritis,
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC multiple sclerosis. The present sequence represents a human anti-TNFa
CC antibody heavy chain variable region, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 125 AA;

Query Match 89.7%; Score 545.5; DB 8; Length 125;
Best Local Similarity 90.4%; Pred. No. 1.5e-42;
Matches 104; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

```
Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||| |||||||||||||||:|||||| |||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAIISYDGSIKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||:  :: || ||:|||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARENAVTYGG-YYHYGMDV 114
```

RESULT 24
ADP22312
ID ADP22312 standard; protein; 125 AA.
XX
AC ADP22312;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human anti-TNFa antibody heavy chain variable region SEQ ID NO:218.
XX
KW human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
KW anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;
KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
KW prostrate cancer; immuno-mediated inflammatory disease;
KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
KW septic shock; cachexia; anorexia; multiple sclerosis.
XX
OS Homo sapiens.
XX
PN WO2004050683-A2.
XX
PD 17-JUN-2004.
XX
PF 02-DEC-2003; 2003WO-US038281.
XX
PR 02-DEC-2002; 2002US-0430729P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Babcook JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;
PI Manchulencho K, Faggioni R, Senaldi G, Qiaojuan JS;
XX
DR WPI; 2004-480601/45.
DR N-PSDB; ADP22311.
XX
PT New recombinant human monoclonal antibody that specifically binds to
PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
PT arthritis.
XX
PS Example 10; SEQ ID NO 218; 213pp; English.
XX
CC The present invention describes a human monoclonal antibody (I) that
CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC (M1) the level of TNFa in a patient sample, comprising contacting with
CC (I), and detecting the level of binding between the antibody and TNFa in
CC the sample; (2) a composition comprising the antibody or its functional
CC fragment and a carrier; (3) treating (M2) an animal suffering from a
CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC animal in need of treatment for the disease by administering the human
CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced
CC apoptosis in an animal by selecting an animal in need of treatment for
CC TNFa induced apoptosis by administering the human monoclonal antibody of
CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
CC disorders, immunomodulator, immunosuppressive, nephrotropic,
CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
CC as a TNFa antagonist. The antibody (I) is useful in the preparation of
CC medicament for treating TNF induced apoptosis, neoplastic disease such as
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer, and prostrate cancer; or immuno-mediated inflammatory
CC diseases such as rheumatoid arthritis, glomerulonephritis,
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC multiple sclerosis. The present sequence represents a human anti-TNFa
CC antibody heavy chain variable region, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 125 AA;

Query Match 89.7%; Score 545.5; DB 8; Length 125;
Best Local Similarity 91.3%; Pred. No. 1.5e-42;
Matches 105; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

```
Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||| |||||||||||||||||| ||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||:  ::  | ||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARETTVTKEG-YYYYGMDV 114


RESULT 25
AAM51167
ID   AAM51167 standard; protein; 118 AA.
XX
AC   AAM51167;
XX
DT   10-JUN-2002  (first entry)
XX
DE   Human DP-46 heavy chain variable region.
XX
KW   Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;
KW   complementarity determining region; antirheumatic; antiarthritic;
KW   antiulcer; antiasthmatic; antiallergic; antiinflammatory; antisickling;
KW   antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;
KW   antianginal; cardiant; antibacterial; virucide; fungicide; antileprotic;
KW   protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;
KW   human; diagnosis; therapy; DP-46.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .30
FT                   /label= FR1
FT   Region          31. .35
FT                   /label= CDR1
FT   Region          36. .49
FT                   /label= FR2
FT   Region          50. .66
FT                   /label= CDR2
FT   Region          67. .98
FT                   /label= FR3
FT   Region          99. .107
FT                   /label= CDR3
FT   Region          108. .118
FT                   /label= J6
XX
PN   WO200212502-A2.
XX
PD   14-FEB-2002.
XX
PF   07-AUG-2001; 2001WO-US024785.
XX
PR   07-AUG-2000; 2000US-0223360P.
PR   29-SEP-2000; 2000US-0236826P.
PR   01-AUG-2001; 2001US-00920137.
XX
PA   (CENZ ) CENTOCOR INC.
XX
PI   Giles-Komar J,  Knight DM,  Heavner G,  Scallon B,  Shealy D;
XX
DR   WPI; 2002-217194/27.
DR   N-PSDB; ABL53507.
XX
PT   Novel isolated mammalian anti-tumor necrosis factor antibody, useful for
PT   treating sickle cell anemia, diabetes, atherosclerosis, restenosis,
PT   angina pectoris, myocardial infarction, leprosy.
XX
PS   Example 3; Fig 4; 131pp; English.
XX
CC   The present sequence is that of a human DP-46 heavy chain variable region
CC   encoded by a human germline DP-46 gene in a transgenic mouse used in
CC   human monoclonal antibody (mAb) construction. A GenTNV fusion was
CC   performed using spleen cells from a hybrid mouse containing human
CC   variable and constant region antibody transgenes that was immunised with
CC   recombinant human tumour necrosis factor (TNF) alpha. Human mAbs were
CC   obtained that bound immobilised human TNF alpha with apparently high
CC   avidity. These mAbs had a totally human IgG1, kappa isotype. Their heavy
CC   chain variable region deduced amino acid sequences (see AAM51168-72)
CC   showed high similarity to the DP-46 sequence. The invention provides
CC   isolated human, primate, rodent, mammalian, chimeric, humanised and/or
CC   complementarity determining region (CDR)-grafted anti-TNF antibodies,
CC   immunoglobulins, and cleavage products and variants, as well as anti-TNF
CC   antibody compositions, encoding or complementary nucleic acids, vectors,
CC   host cells, compositions, formulations, devices, transgenic animals,
CC   transgenic plants, and methods of making and using them. The anti-TNF
CC   antibody comprises at least a portion of an immunoglobulin molecule,
CC   especially the heavy chain and/or light chain variable regions given in
CC   the present sequence and in AAM51165, or either all of the CDRs of the
CC   heavy chain (see AAM51158-60) or all of the CDRs of the light chain (see
CC   AAM51161-63). The antibodies may inhibit TNF-induced cell adhesion
CC   molecules, inhibit TNF binding to receptor, or provide Arthritic Index
CC   improvement in a mouse model. They are useful for diagnosing or treating
CC   a TNF related condition in a cell, tissue, organ or animal (claimed) such
CC   as rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis,
CC   Crohn's pathology, sickle cell anaemia, diabetes, a cardiovascular
CC   disease such as arteriosclerosis, atherosclerosis, restenosis, angina
CC   pectoris or myocardial infarction, an infectious disease in a cell such
CC   as bacterial, viral, and fungal infections, pneumonia, leprosy and
CC   malaria, a malignant disease such as leukaemia, chronic myelocytic
CC   leukaemia, Burkitt's lymphoma and multiple myeloma, or a neurological
CC   disease such as multiple sclerosis, Parkinson's disease, spinal ataxia,
CC   Alzheimer's disease and Creutzfeldt-Jakob disease
XX
SQ   Sequence 118 AA;

  Query Match             89.6%;  Score 545;  DB 5;  Length 118;
  Best Local Similarity   92.2%;  Pred. No. 1.6e-42;
  Matches  106;  Conservative    0;  Mismatches    1;  Indels    8;  Gaps    1;

Qy          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYY 60

Qy         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGISAGGNYYYYGMDV 115
              |||||||||||||||||||||||||||||||||||||||||         ||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR--------YYYYYGMDV 107


Search completed: June 16, 2005, 07:42:59
Job time : 126.188 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 07:35:01 ; Search time 29.5426 Seconds
(without alignments)
272.897 Million cell updates/sec

Title: US-09-920-137D-8
Perfect score: 565
Sequence: 1 EIVLTQSPATLSLSPGERAT.....QQRSNWPPFTFGPGTKVDIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	529.5	93.7	224	4	US-09-456-090A-46	Sequence 46, Appl
2	529.5	93.7	224	4	US-09-453-234-46	Sequence 46, Appl
3	524.5	92.8	224	4	US-09-456-090A-82	Sequence 82, Appl
4	524.5	92.8	224	4	US-09-456-090A-88	Sequence 88, Appl
5	524.5	92.8	224	4	US-09-456-090A-90	Sequence 90, Appl
6	524.5	92.8	224	4	US-09-453-234-82	Sequence 82, Appl
7	524.5	92.8	224	4	US-09-453-234-88	Sequence 88, Appl
8	524.5	92.8	224	4	US-09-453-234-90	Sequence 90, Appl
9	523.5	92.7	224	4	US-09-456-090A-36	Sequence 36, Appl
10	523.5	92.7	224	4	US-09-453-234-36	Sequence 36, Appl
11	520.5	92.1	224	4	US-09-456-090A-84	Sequence 84, Appl
12	520.5	92.1	224	4	US-09-453-234-84	Sequence 84, Appl
13	515.5	91.2	107	4	US-09-438-954-40	Sequence 40, Appl
14	499.5	88.4	226	4	US-09-456-090A-38	Sequence 38, Appl
15	499.5	88.4	226	4	US-09-453-234-38	Sequence 38, Appl
16	495	87.6	117	4	US-09-203-768A-4	Sequence 4, Appli
17	493	87.3	115	1	US-08-053-131-179	Sequence 179, App
18	493	87.3	115	2	US-08-096-762-179	Sequence 179, App
19	493	87.3	115	3	US-09-042-353-42	Sequence 42, Appl
20	493	87.3	115	3	US-08-758-417A-307	Sequence 307, App
21	492	87.1	105	4	US-08-635-109-6	Sequence 6, Appli
22	492	87.1	105	4	US-08-844-215-9	Sequence 9, Appli
23	491.5	87.0	226	4	US-09-456-090A-72	Sequence 72, Appl
24	491.5	87.0	226	4	US-09-453-234-72	Sequence 72, Appl
25	485.5	85.9	226	4	US-09-456-090A-42	Sequence 42, Appl
26	485.5	85.9	226	4	US-09-453-234-42	Sequence 42, Appl
27	480	85.0	110	3	US-09-025-769B-30	Sequence 30, Appl
28	480	85.0	110	3	US-09-025-769B-47	Sequence 47, Appl
29	480	85.0	110	4	US-09-490-070A-30	Sequence 30, Appl
30	480	85.0	110	4	US-09-490-070A-47	Sequence 47, Appl
31	480	85.0	110	4	US-09-490-153-30	Sequence 30, Appl
32	480	85.0	110	4	US-09-490-153-47	Sequence 47, Appl
33	480	85.0	110	4	US-09-490-324-30	Sequence 30, Appl
34	480	85.0	110	4	US-09-490-324-47	Sequence 47, Appl
35	479.5	84.9	226	4	US-09-456-090A-50	Sequence 50, Appl
36	479.5	84.9	226	4	US-09-456-090A-86	Sequence 86, Appl
37	479.5	84.9	226	4	US-09-453-234-50	Sequence 50, Appl
38	479.5	84.9	226	4	US-09-453-234-86	Sequence 86, Appl
39	478.5	84.7	226	4	US-09-456-090A-74	Sequence 74, Appl
40	478.5	84.7	226	4	US-09-453-234-74	Sequence 74, Appl
41	477.5	84.5	234	4	US-09-472-087-17	Sequence 17, Appl
42	477.5	84.5	234	4	US-09-472-087-69	Sequence 69, Appl
43	477	84.4	115	1	US-08-053-131-181	Sequence 181, App
44	477	84.4	115	2	US-08-096-762-181	Sequence 181, App
45	477	84.4	115	3	US-09-042-353-44	Sequence 44, Appl
46	477	84.4	115	3	US-08-758-417A-309	Sequence 309, App
47	474.5	84.0	224	4	US-09-456-090A-52	Sequence 52, Appl
48	474.5	84.0	224	4	US-09-453-234-52	Sequence 52, Appl
49	472	83.5	109	3	US-09-025-769B-16	Sequence 16, Appl
50	472	83.5	109	4	US-09-490-070A-16	Sequence 16, Appl
51	472	83.5	109	4	US-09-490-153-16	Sequence 16, Appl
52	472	83.5	109	4	US-09-490-324-16	Sequence 16, Appl
53	470.5	83.3	224	4	US-09-456-090A-44	Sequence 44, Appl
54	470.5	83.3	224	4	US-09-456-090A-78	Sequence 78, Appl
55	470.5	83.3	224	4	US-09-453-234-44	Sequence 44, Appl
56	470.5	83.3	224	4	US-09-453-234-78	Sequence 78, Appl
57	469.5	83.1	146	4	US-09-472-087-21	Sequence 21, Appl
58	469.5	83.1	146	4	US-09-472-087-93	Sequence 93, Appl
59	467.5	82.7	226	4	US-09-456-090A-80	Sequence 80, Appl
60	467.5	82.7	226	4	US-09-453-234-80	Sequence 80, Appl
61	465.5	82.4	224	4	US-09-456-090A-40	Sequence 40, Appl
62	465.5	82.4	224	4	US-09-453-234-40	Sequence 40, Appl
63	463.5	82.0	224	4	US-09-456-090A-76	Sequence 76, Appl
64	463.5	82.0	224	4	US-09-453-234-76	Sequence 76, Appl
65	461	81.6	108	2	US-08-232-081B-42	Sequence 42, Appl
66	460.5	81.5	107	1	US-08-107-669D-14	Sequence 14, Appl
67	460.5	81.5	107	1	US-08-472-788A-14	Sequence 14, Appl
68	460.5	81.5	107	2	US-08-477-531B-14	Sequence 14, Appl
69	460.5	81.5	107	2	US-08-082-842A-14	Sequence 14, Appl
70	458.5	81.2	107	3	US-09-247-352-12	Sequence 12, Appl
71	457.5	81.0	107	3	US-09-247-352-8	Sequence 8, Appli
72	456.5	80.8	100	4	US-09-899-896-2	Sequence 2, Appli
73	456	80.7	108	1	US-08-488-113B-150	Sequence 150, App
74	456	80.7	108	1	US-08-477-484B-150	Sequence 150, App
75	456	80.7	108	2	US-08-646-360-150	Sequence 150, App
76	456	80.7	108	3	US-08-839-765-150	Sequence 150, App
77	456	80.7	108	3	US-09-136-389-150	Sequence 150, App
78	456	80.7	108	3	US-09-610-838-150	Sequence 150, App
79	456	80.7	108	4	US-09-711-485-150	Sequence 150, App
80	456	80.7	235	4	US-09-472-087-14	Sequence 14, Appl
81	456	80.7	235	4	US-09-472-087-65	Sequence 65, Appl
82	455.5	80.6	142	4	US-09-472-087-91	Sequence 91, Appl
83	453.5	80.3	139	4	US-09-472-087-16	Sequence 16, Appl
84	453.5	80.3	139	4	US-09-472-087-90	Sequence 90, Appl
85	453	80.2	150	3	US-08-862-124-5	Sequence 5, Appli
86	453	80.2	287	3	US-08-862-124-17	Sequence 17, Appl
87	453	80.2	304	3	US-08-862-124-14	Sequence 14, Appl
88	451.5	79.9	100	4	US-09-899-896-4	Sequence 4, Appli
89	451	79.8	108	3	US-09-240-274-178	Sequence 178, App
90	450	79.6	233	4	US-09-472-087-15	Sequence 15, Appl
91	450	79.6	233	4	US-09-472-087-67	Sequence 67, Appl
92	449.5	79.6	236	4	US-09-859-053-34	Sequence 34, Appl
93	448	79.3	108	1	US-07-634-278-86	Sequence 86, Appl
94	448	79.3	108	1	US-08-477-728-86	Sequence 86, Appl
95	448	79.3	108	1	US-08-474-040-86	Sequence 86, Appl
96	448	79.3	108	1	US-08-487-200-86	Sequence 86, Appl
97	448	79.3	108	3	US-08-484-537-86	Sequence 86, Appl
98	447.5	79.2	107	4	US-09-339-922A-32	Sequence 32, Appl
99	447.5	79.2	107	4	US-08-791-391A-32	Sequence 32, Appl
100	447.5	79.2	107	4	US-09-016-061-32	Sequence 32, Appl

ALIGNMENTS

```
RESULT 1
US-09-456-090A-46
; Sequence 46, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M1-10L
US-09-456-090A-46

  Query Match             93.7%;  Score 529.5;  DB 4;  Length 224;
  Best Local Similarity   94.4%;  Pred. No. 6.3e-43;
  Matches  102;  Conservative    4;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ::|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DVVMTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||||| ||| ||||:||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPP-TFGGGTKVEIK 107


RESULT 2
US-09-453-234-46
; Sequence 46, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M1-10L
US-09-453-234-46

  Query Match             93.7%;  Score 529.5;  DB 4;  Length 224;
  Best Local Similarity   94.4%;  Pred. No. 6.3e-43;
  Matches  102;  Conservative    4;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ::|:||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DVVMTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||||| ||| ||||:||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPP-TFGGGTKVEIK 107


RESULT 3
US-09-456-090A-82
; Sequence 82, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-31L
US-09-456-090A-82

  Query Match             92.8%;  Score 524.5;  DB 4;  Length 224;
  Best Local Similarity   95.4%;  Pred. No. 1.9e-42;
  Matches  103;  Conservative    2;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||:|||  ||| ||||:||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRTNWPR-TFGQGTKVEIK 107


RESULT 4
US-09-456-090A-88
; Sequence 88, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-34L
US-09-456-090A-88

  Query Match             92.8%;  Score 524.5;  DB 4;  Length 224;
  Best Local Similarity   95.4%;  Pred. No. 1.9e-42;
  Matches  103;  Conservative    2;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||:|||  ||| ||||:||
```

```
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRTNWPR-TFGQGTKVEIK 107


RESULT 5
US-09-456-090A-90
; Sequence 90, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-35L
US-09-456-090A-90

  Query Match            92.8%;  Score 524.5;  DB 4;  Length 224;
  Best Local Similarity  95.4%;  Pred. No. 1.9e-42;
  Matches  103;  Conservative    2;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||:|||  ||| ||||:||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRTNWPR-TFGQGTKVEIK 107


RESULT 6
US-09-453-234-82
; Sequence 82, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-31L
US-09-453-234-82

  Query Match            92.8%;  Score 524.5;  DB 4;  Length 224;
  Best Local Similarity  95.4%;  Pred. No. 1.9e-42;
  Matches  103;  Conservative    2;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||:|||  ||| ||||:||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRTNWPR-TFGQGTKVEIK 107


RESULT 7
US-09-453-234-88
; Sequence 88, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-34L
US-09-453-234-88

  Query Match            92.8%;  Score 524.5;  DB 4;  Length 224;
  Best Local Similarity  95.4%;  Pred. No. 1.9e-42;
  Matches  103;  Conservative    2;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||:|||  ||| ||||:||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRTNWPR-TFGQGTKVEIK 107


RESULT 8
US-09-453-234-90
; Sequence 90, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-35L
US-09-453-234-90

  Query Match            92.8%;  Score 524.5;  DB 4;  Length 224;
  Best Local Similarity  95.4%;  Pred. No. 1.9e-42;
  Matches  103;  Conservative    2;  Mismatches    2;  Indels    1;  Gaps    1;
```

```
Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||:|||  ||| ||||:||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRTNWPR-TFGQGTKVEIK 107


RESULT 9
US-09-456-090A-36
; Sequence 36, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: M1-1L
US-09-456-090A-36

  Query Match             92.7%;  Score 523.5;  DB 4;  Length 224;
  Best Local Similarity   95.4%;  Pred. No. 2.3e-42;
  Matches  103;  Conservative    1;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQGVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||  ||| ||||:||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPR-TFGQGTKVEIK 107


RESULT 10
US-09-453-234-36
; Sequence 36, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-453-234-36

  Query Match             92.7%;  Score 523.5;  DB 4;  Length 224;
  Best Local Similarity   95.4%;  Pred. No. 2.3e-42;
  Matches  103;  Conservative    1;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQGVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||||  ||| ||||:||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPR-TFGQGTKVEIK 107


RESULT 11
US-09-456-090A-84
; Sequence 84, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-32L
US-09-456-090A-84

  Query Match             92.1%;  Score 520.5;  DB 4;  Length 224;
  Best Local Similarity   94.4%;  Pred. No. 4.5e-42;
  Matches  102;  Conservative    2;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRAAGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||:|| | ||| ||||:||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRNNW-PLTFGGGTKVEIK 107


RESULT 12
US-09-453-234-84
; Sequence 84, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
;   LENGTH: 224
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-32L
US-09-453-234-84

  Query Match             92.1%;  Score 520.5;  DB 4;  Length 224;
  Best Local Similarity   94.4%;  Pred. No. 4.5e-42;
```

Matches 102; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

```
Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRAAGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||:|| | ||| ||||:||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRNNW-PLTFGGGTKVEIK 107
```

RESULT 13
US-09-438-954-40
; Sequence 40, Application US/09438954
; Patent No. 6458934
; GENERAL INFORMATION:
; APPLICANT: HONG, Hyo Jeong
; APPLICANT: PARK, Sung Sup
; APPLICANT: KANG, Young Jun
; APPLICANT: KANG, Chang-Yuil
; APPLICANT: YOON, Sung Kwan
; TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR HUMAN 4-1BB AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING SAME
; FILE REFERENCE: 1303-124P
; CURRENT APPLICATION NUMBER: US/09/438,954
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Variable
; OTHER INFORMATION: region of light chain of human antibody (X82934)
US-09-438-954-40

Query Match 91.2%; Score 515.5; DB 4; Length 107;
Best Local Similarity 91.7%; Pred. No. 6e-42;
Matches 99; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

```
Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ::|:|||||||||:|||||||||||||||||||||||||||||||||||| |||||||
Db          1 DVVMTQSPATLSVSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASRRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||| ||||||| ||| ||||:||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYC-QRSNWPPLTFGGGTKVEIK 107
```

RESULT 14
US-09-456-090A-38
; Sequence 38, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-3L
US-09-456-090A-38

Query Match 88.4%; Score 499.5; DB 4; Length 226;
Best Local Similarity 90.8%; Pred. No. 4.5e-40;
Matches 99; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

```
Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQKPGQAPRLLIYDASNRATGIP 59
              |||:|||||||||||||||||||||||| |||||||||||||||||| ||:||||||
Db          1 EIVMTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||| |||||||||||| : |||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPFTFGPGTKVDIK 109
```

RESULT 15
US-09-453-234-38
; Sequence 38, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-3L
US-09-453-234-38

Query Match 88.4%; Score 499.5; DB 4; Length 226;
Best Local Similarity 90.8%; Pred. No. 4.5e-40;
Matches 99; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

```
Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQKPGQAPRLLIYDASNRATGIP 59
              |||:|||||||||||||||||||||||| |||||||||||||||||| ||:||||||
Db          1 EIVMTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||| |||||||||||| : |||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPFTFGPGTKVDIK 109
```

RESULT 16
US-09-203-768A-4
; Sequence 4, Application US/09203768A
; Patent No. 6787638
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Watkins, Jeffry D.
; TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: P-IX 2947
; CURRENT APPLICATION NUMBER: US/09/203,768A
; CURRENT FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-203-768A-4

Query Match 87.6%; Score 495; DB 4; Length 117;
Best Local Similarity 87.0%; Pred. No. 5.9e-40;

```
  Matches   94;  Conservative    8;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              |||:||||||||:|||||||||||||||||| |||||||||||||||| || |||||||
Db          9 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 68

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||:||||||||: |||||||||| :||||:||| |||::||
Db         69 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPPYTFGQGTKLEIK 116


RESULT 17
US-08-053-131-179
; Sequence 179, Application US/08053131
; Patent No. 5661016
;  GENERAL INFORMATION:
;    APPLICANT:  Lonberg, Nils
;    APPLICANT:  Kay, Robert M.
;    TITLE OF INVENTION:  Transgenic No. 5661016-Human Animals for
;    TITLE OF INVENTION:  Producing Heterologous Antibodies
;    NUMBER OF SEQUENCES:  197
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/053,131
;      FILING DATE:  26-APR-1993
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/990,860
;      FILING DATE:  16-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/810,279
;      FILING DATE:  17-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/853,408
;      FILING DATE:  18-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  14643-9-3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  179:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  115 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-053-131-179

  Query Match             87.3%;  Score 493;  DB 1;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-40;
  Matches   95;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWP 95
              |||||||||||||||||||||||||||||||||||
Db         81 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWP 115


RESULT 18
US-08-096-762-179
; Sequence 179, Application US/08096762
; Patent No. 5814318
;  GENERAL INFORMATION:
;    APPLICANT:  Lonberg, Nils
;    APPLICANT:  Kay, Robert M.
;    TITLE OF INVENTION:  Transgenic No. 5814318-Human Animals for
;    TITLE OF INVENTION:  Producing Heterologous Antibodies
;    NUMBER OF SEQUENCES:  210
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/096,762
;      FILING DATE:  22-JUL-1993
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/053,131
;      FILING DATE:  26-APR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/990,860
;      FILING DATE:  16-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/904,068
;      FILING DATE:  23-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/853,408
;      FILING DATE:  18-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/810,279
;      FILING DATE:  17-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  14643-9-4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  179:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  115 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-096-762-179

  Query Match             87.3%;  Score 493;  DB 2;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-40;
  Matches   95;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWP 95
              |||||||||||||||||||||||||||||||||||
Db         81 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWP 115


RESULT 19
US-09-042-353-42
; Sequence 42, Application US/09042353
```

```
; Patent No. 6255458
;  GENERAL INFORMATION:
;    APPLICANT:  Lonberg, Nils
;    APPLICANT:  Kay, Robert M.
;    TITLE OF INVENTION:  Transgenic No. 6255458-Human Animals for
;    TITLE OF INVENTION:  Producing Heterologous Antibodies
;    NUMBER OF SEQUENCES:  421
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/042,353
;      FILING DATE:  13-MAR-1998
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/810,279
;      FILING DATE:  17-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/853,408
;      FILING DATE:  18-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/904,068
;      FILING DATE:  23-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/990,860
;      FILING DATE:  16-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/053,131
;      FILING DATE:  26-APR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/096,762
;      FILING DATE:  22-JUL-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/155,301
;      FILING DATE:  18-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/161,739
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/165,699
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/209,741
;      FILING DATE:  09-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/352,322
;      FILING DATE:  07-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/544,404
;      FILING DATE:  10-OCT-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/728,463
;      FILING DATE:  10-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US96/16433
;      FILING DATE:  10-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/758,417
;      FILING DATE:  02-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/21803
;      FILING DATE:  01-DEC-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Apple, Randolph T.
;      REGISTRATION NUMBER:  36,429
;      REFERENCE/DOCKET NUMBER:  014643-009040US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  115 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-042-353-42

  Query Match          87.3%;  Score 493;  DB 3;  Length 115;
  Best Local Similarity  100.0%;  Pred. No. 8.9e-40;
  Matches   95;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWP 95
              |||||||||||||||||||||||||||||||||||
Db         81 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWP 115


RESULT 20
US-08-758-417A-307
; Sequence 307, Application US/08758417A
; Patent No. 6300129
;   GENERAL INFORMATION:
;        APPLICANT: Lonberg, Nils
;                   Kay, Robert M.
;        TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
;                            Producing Heterologous Antibodies
;        NUMBER OF SEQUENCES: 417
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/758,417A
;             FILING DATE: 02-Dec-1996
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/728,463
;             FILING DATE: 10-OCT-1996
;             APPLICATION NUMBER: US 08/544,404
;             FILING DATE: 10-OCT-1995
;             APPLICATION NUMBER: US 08/352,322
;             FILING DATE: 07-DEC-1994
;             APPLICATION NUMBER: US 08/209,741
;             FILING DATE: 09-MAR-1994
;             APPLICATION NUMBER: US 08/165,699
;             FILING DATE: 10-DEC-1993
;             APPLICATION NUMBER: US 08/161,739
;             FILING DATE: 03-DEC-1993
;             APPLICATION NUMBER: US 08/155,301
;             FILING DATE: 18-NOV-1993
;             APPLICATION NUMBER: US 08/096,762
;             FILING DATE: 22-JUL-1993
;             APPLICATION NUMBER: US 08/053,131
;             FILING DATE: 26-APR-1993
;             APPLICATION NUMBER: US 07/990,860
;             FILING DATE: 16-DEC-1992
```

```
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Serafini, Andrew T.
;            REGISTRATION NUMBER: 41,303
;            REFERENCE/DOCKET NUMBER: 014643-009030US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 307:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 115 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 307:
US-08-758-417A-307

  Query Match             87.3%;  Score 493;  DB 3;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-40;
  Matches   95;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWP 95
              |||||||||||||||||||||||||||||||||||
Db         81 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWP 115


RESULT 21
US-08-635-109-6
; Sequence 6, Application US/08635109
; Patent No. 6538114
;  GENERAL INFORMATION:
;    APPLICANT:  Persson, Mats A. A.
;    APPLICANT:  Allander, Tobias E.
;    TITLE OF INVENTION:  HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
;    TITLE OF INVENTION:  HEPATITIS C VIRUS (HCV) E2 ANTIGEN
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  REED & ROBINS
;      STREET:  285 Hamilton Avenue, Suite 200
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/635,109
;      FILING DATE:  19-APR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McCracken, Thomas P
;      REGISTRATION NUMBER:  38,548
;      REFERENCE/DOCKET NUMBER:  2300-6146
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 327-3400
;      TELEFAX:  (415) 327-3231
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  105 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-635-109-6

  Query Match             87.1%;  Score 492;  DB 4;  Length 105;
  Best Local Similarity   91.4%;  Pred. No. 1e-39;
  Matches   96;  Conservative    4;  Mismatches    3;  Indels    2;  Gaps    1;

Qy          4 LTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFS 63
              |||||||||||||||||||||||||: ||||||||||||||||||||||||||||||||
Db          3 LTQSPATLSLSPGERATLSCRASQSVNKYLAWYQQKPGQAPRLLIYDASNRATGIPARFS 62

Qy         64 GSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||:|||||||||||||||:|   ||| ||||:||
Db         63 GSGSGTDFTLTISNLEPEDFAVYYCQQRSDW--VTFGGGTKVEIK 105


RESULT 22
US-08-844-215-9
; Sequence 9, Application US/08844215
; Patent No. 6747136
;  GENERAL INFORMATION:
;    APPLICANT:  PERSSON, MATS AXEL
;    APPLICANT:  ALLANDER, TOBIAS ERIK
;    TITLE OF INVENTION:  HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
;    TITLE OF INVENTION:  HEPATITIS C VIRUS (HCV) E2 ANTIGEN
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROBINS & ASSOCIATES
;      STREET:  90 MIDDLEFIELD ROAD, SUITE 200
;      CITY:  MENLO PARK
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/844,215
;      FILING DATE:  17-APR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/635,109
;      FILING DATE:  19-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MCCRACKEN, THOMAS P.
;      REGISTRATION NUMBER:  38,548
;      REFERENCE/DOCKET NUMBER:  80146.002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 325-7812
;      TELEFAX:  (650) 325-7823
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  105 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-844-215-9

  Query Match             87.1%;  Score 492;  DB 4;  Length 105;
  Best Local Similarity   91.4%;  Pred. No. 1e-39;
  Matches   96;  Conservative    4;  Mismatches    3;  Indels    2;  Gaps    1;

Qy          4 LTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFS 63
              |||||||||||||||||||||||||: ||||||||||||||||||||||||||||||||
Db          3 LTQSPATLSLSPGERATLSCRASQSVNKYLAWYQQKPGQAPRLLIYDASNRATGIPARFS 62

Qy         64 GSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||:|||||||||||||||:|   ||| ||||:||
Db         63 GSGSGTDFTLTISNLEPEDFAVYYCQQRSDW--VTFGGGTKVEIK 105


RESULT 23
US-09-456-090A-72
; Sequence 72, Application US/09456090A
; Patent No. 6680209
```

```
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-11L
US-09-456-090A-72

  Query Match             87.0%;  Score 491.5;  DB 4;  Length 226;
  Best Local Similarity   89.0%;  Pred. No. 2.6e-39;
  Matches   97;  Conservative    3;  Mismatches    8;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQKPGQAPRLLIYDASNRATGIP 59
              |||:|||| |||||||||||||||||| | |||||||||||||||||| ||:||||||
Db          1 EIVMTQSPGTLSLSPGERATLSCRASQGVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
               |||||||||||||||| ||||||||||||  : |||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPFTFGPGTKVDIK 109


RESULT 24
US-09-453-234-72
; Sequence 72, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M2-11L
US-09-453-234-72

  Query Match             87.0%;  Score 491.5;  DB 4;  Length 226;
  Best Local Similarity   89.0%;  Pred. No. 2.6e-39;
  Matches   97;  Conservative    3;  Mismatches    8;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQKPGQAPRLLIYDASNRATGIP 59
              |||:|||| |||||||||||||||||| | |||||||||||||||||| ||:||||||
Db          1 EIVMTQSPGTLSLSPGERATLSCRASQGVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
               |||||||||||||||| ||||||||||||  : |||||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPFTFGPGTKVDIK 109


RESULT 25
US-09-456-090A-42
; Sequence 42, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
;   LENGTH: 226
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   OTHER INFORMATION: M1-5L
US-09-456-090A-42

  Query Match             85.9%;  Score 485.5;  DB 4;  Length 226;
  Best Local Similarity   89.0%;  Pred. No. 9.7e-39;
  Matches   97;  Conservative    3;  Mismatches    8;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQKPGQAPRLLIYDASNRATGIP 59
              |||:|||| |||||||||||||||||| |||||||||||||||||| ||:||||||
Db          1 EIVMTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
               |||||||||||||||| ||||||||||||  : | ||||||||||||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPIFTFGPGTKVDIK 109


Search completed: June 16, 2005, 07:44:05
Job time : 31.5426 secs
```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 07:35:01 ; Search time 113.812 Seconds
(without alignments)
367.011 Million cell updates/sec

Title: US-09-920-137D-8
Perfect score: 565
Sequence: 1 EIVLTQSPATLSLSPGERAT.....QQRSNWPPFTFGPGTKVDIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	565	100.0	108	5	AAM51165	Aam51165 Anti-tumo
2	565	100.0	108	5	AAM51173	Aam51173 Human Vg/
3	565	100.0	108	5	AAU76334	Aau76334 Human ant
4	565	100.0	108	7	ADJ73533	Adj73533 Erythropo
5	565	100.0	108	7	ADJ73534	Adj73534 Erythropo
6	565	100.0	129	5	AAM51174	Aam51174 Human rec
7	565	100.0	129	5	AAM51175	Aam51175 Human mAb
8	547	96.8	108	4	AAB72884	Aab72884 Human ant
9	547	96.8	109	7	ADF11411	Adf11411 16E1 anti
10	547	96.8	215	7	ADF11435	Adf11435 16E1 anti
11	546	96.6	128	8	ADM41547	Adm41547 Anti-inte
12	546	96.6	130	7	ADD89877	Add89877 Human ant
13	546	96.6	130	8	ADS64664	Ads64664 Human 9E7
14	546	96.6	130	8	ADS64653	Ads64653 Human ant
15	546	96.6	235	8	ADM41573	Adm41573 Anti-inte
16	544	96.3	108	8	ADS19298	Ads19298 Light cha
17	542	95.9	109	7	ADF11395	Adf11395 22B3 anti
18	542	95.9	215	7	ADF11419	Adf11419 22B3 anti
19	541	95.8	108	8	ADI22138	Adi22138 Anti-plat
20	540	95.6	109	7	ADF11403	Adf11403 2D8 anti-
21	540	95.6	109	7	ADF11415	Adf11415 9H7 anti-
22	540	95.6	215	7	ADF11439	Adf11439 9H7 anti-
23	540	95.6	215	7	ADF11427	Adf11427 2D8 anti-
24	537.5	95.1	129	6	ABP57362	Abp57362 Anti-TRAI
25	535.5	94.8	107	6	ABR54916	Abr54916 Light cha
26	535	94.7	251	5	ABP45038	Abp45038 Human BLy
27	535	94.7	251	7	ADG95865	Adg95865 Single ch
28	534.5	94.6	129	7	ADJ73532	Adj73532 Erythropo
29	533	94.3	128	7	ADJ73528	Adj73528 Erythropo
30	531	94.0	109	4	AAB62756	Aab62756 Human HIV
31	530.5	93.9	214	8	ADH34591	Adh34591 023 light
32	529.5	93.7	224	4	AAB99371	Aab99371 Human int
33	529.5	93.7	224	4	AAB75004	Aab75004 Anti-IL8
34	529	93.6	130	8	ADH17916	Adh17916 Human 1H3
35	528.5	93.5	107	4	AAB80988	Aab80988 Human ant
36	528.5	93.5	128	6	ABP57368	Abp57368 Anti-TRAI
37	528.5	93.5	139	8	ADS88106	Ads88106 Human CD2
38	528	93.5	106	8	ADI22136	Adi22136 Anti-plat
39	528	93.5	108	7	ADD69213	Add69213 Human ant
40	526.5	93.2	107	8	ADI22135	Adi22135 Anti-plat
41	526.5	93.2	129	6	ABP57364	Abp57364 Anti-TRAI
42	524.5	92.8	224	4	AAB99399	Aab99399 Human int
43	524.5	92.8	224	4	AAB99395	Aab99395 Human int
44	524.5	92.8	224	4	AAB99398	Aab99398 Human int
45	524.5	92.8	224	4	AAB75031	Aab75031 Anti-IL8
46	524.5	92.8	224	4	AAB75028	Aab75028 Anti-IL8
47	524.5	92.8	224	4	AAB75032	Aab75032 Anti-IL8
48	524.5	92.8	247	8	ADH34575	Adh34575 scFv SC02
49	524.5	92.8	247	8	ADH34573	Adh34573 scFv SC02
50	524	92.7	108	7	ADD69212	Add69212 Human ant
51	524	92.7	108	8	ADS19308	Ads19308 Light cha
52	523.5	92.7	107	6	ABR54917	Abr54917 Light cha
53	523.5	92.7	127	8	ADS88059	Ads88059 Human CD2
54	523.5	92.7	127	8	ADS88063	Ads88063 Human CD2
55	523.5	92.7	127	8	ADS88108	Ads88108 Human CD2
56	523.5	92.7	127	8	ADS88055	Ads88055 Human CD2
57	523.5	92.7	224	4	AAB99372	Aab99372 Human int
58	523.5	92.7	224	4	AAB75005	Aab75005 Anti-IL8
59	523	92.6	108	7	ADD69214	Add69214 Human ant
60	522	92.4	126	6	ABJ36922	Abj36922 Anti-CD40
61	521.5	92.3	107	5	ABB07235	Abb07235 Anti-IL-4
62	520.5	92.1	224	4	AAB99396	Aab99396 Human int
63	520.5	92.1	224	4	AAB75029	Aab75029 Anti-IL8
64	519.5	91.9	219	4	AAG71321	Aag71321 Human gen
65	517.5	91.6	107	4	AAB85350	Aab85350 Antibody
66	516.5	91.4	107	6	ABR54915	Abr54915 Light cha
67	516	91.3	129	6	ABJ36924	Abj36924 Anti-CD40
68	515.5	91.2	107	6	AAE38061	Aae38061 Human 2H9
69	514.5	91.1	109	6	ABP96283	Abp96283 Anti-hTNF
70	514.5	91.1	119	6	ABP96292	Abp96292 Human ant
71	514.5	91.1	214	6	ABP96296	Abp96296 4A5-3.1.1
72	513.5	90.9	107	8	ADO07301	Ado07301 Human pro
73	513.5	90.9	214	2	AAY08599	Aay08599 Anti-huma
74	513.5	90.9	224	4	AAB75036	Aab75036 TRO005 Hu
75	513.5	90.9	224	4	AAB75034	Aab75034 TRO005 Hu
76	513.5	90.9	224	4	AAB75037	Aab75037 TRO005 Hu
77	513.5	90.9	259	4	AAM23532	Aam23532 Human EST
78	513.5	90.9	349	2	AAR12128	Aar12128 1B1 IgG a
79	513.5	90.9	401	2	AAR12129	Aar12129 ORF 1 of
80	513.5	90.9	414	2	AAR13111	Aar13111 1B1 IgG a
81	513.5	90.9	414	2	AAR13018	Aar13018 1B1 IgG a
82	512.5	90.7	156	4	AAG71323	Aag71323 Human gen
83	512	90.6	109	6	ADA89232	Ada89232 Human ant
84	512	90.6	109	6	ADA89228	Ada89228 Human ant
85	511.5	90.5	107	4	AAB66414	Aab66414 Human Fab
86	510.5	90.4	245	8	ADI58105	Adi58105 Reg IV-sp
87	508.5	90.0	236	4	AAG71272	Aag71272 Human gen
88	508.5	90.0	236	5	ABG63490	Abg63490 Human alb
89	508.5	90.0	236	8	ADL76755	Adl76755 Albumin f
90	506.5	89.6	131	7	ADJ73531	Adj73531 Erythropo
91	506.5	89.6	214	8	ADL70802	Adl70802 Anti-TNFa
92	506.5	89.6	214	8	ADL70799	Adl70799 Anti-TNFa
93	504.5	89.3	234	6	ABP55483	Abp55483 CJRA05 pr
94	503	89.0	125	6	ABJ36934	Abj36934 Anti-CD40
95	501.5	88.8	224	4	AAB75039	Aab75039 TRO005 Hu
96	499.5	88.4	226	4	AAB99376	Aab99376 Human int
97	499.5	88.4	226	4	AAB75009	Aab75009 Anti-IL8
98	498.5	88.2	107	6	ABR55830	Abr55830 Kappa cha

99	497.5	88.1	110	8	ADP47298	Adp47298 Human pho
100	497.5	88.1	234	5	AAO14066	Aao14066 Light cha

ALIGNMENTS

RESULT 1
AAM51165
ID AAM51165 standard; protein; 108 AA.
XX
AC AAM51165;
XX
DT 10-JUN-2002 (first entry)
XX
DE Anti-tumour necrosis factor antibody light chain variable region.
XX
KW Tumour necrosis factor alpha; TNF; antibody; light chain; CDR;
KW complementarity determining region; antirheumatic; antiarthritic;
KW antiulcer; antiasthmatic; antiallergic; antiinflammatory; antisickling;
KW antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;
KW antianginal; cardiant; antibacterial; virucide; fungicide; antileprotic;
KW protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;
KW human; diagnosis; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1. .23
FT /label= FR1
FT Region 24. .34
FT /label= CDR1
FT Region 35. .49
FT /label= FR2
FT Region 50. .56
FT /label= CDR2
FT Region 57. .88
FT /label= FR3
FT Region 89. .98
FT /label= CDR3
FT Region 99. .108
FT /label= J6
XX
PN WO200212502-A2.
XX
PD 14-FEB-2002.
XX
PF 07-AUG-2001; 2001WO-US024785.
XX
PR 07-AUG-2000; 2000US-0223360P.
PR 29-SEP-2000; 2000US-0236826P.
PR 01-AUG-2001; 2001US-00920137.
XX
PA (CENZ) CENTOCOR INC.
XX
PI Giles-Komar J, Knight DM, Heavner G, Scallon B, Shealy D;
XX
DR WPI; 2002-217194/27.
XX
PT Novel isolated mammalian anti-tumor necrosis factor antibody, useful for
PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,
PT angina pectoris, myocardial infarction, leprosy.
XX
PS Claim 9; Page 129-130; 131pp; English.
XX
CC The present sequence is that of the light chain variable region of an
CC anti-tumour necrosis factor (TNF) antibody of the invention. The
CC invention provides isolated human, primate, rodent, mammalian, chimeric,
CC humanised and/or complementarity determining region (CDR)-grafted anti-
CC TNF antibodies, immunoglobulins, cleavage products and other specified
CC portions and variants, as well as anti-TNF antibody compositions,
CC encoding or complementary nucleic acids, vectors, host cells,
CC compositions, formulations, devices, transgenic animals, transgenic
CC plants, and methods of making and using them. The anti-TNF antibody
CC comprises at least a portion of an immunoglobulin molecule, especially
CC the heavy chain and/or light chain variable regions given in AAM51164 and
CC in the present sequence, or either all of the CDRs of the heavy chain
CC (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-
CC 63). The antibody may inhibit TNF-induced cell adhesion molecules,
CC inhibit TNF binding to receptor, or provide Arthritic Index improvement
CC in a mouse model. It is useful for diagnosing or treating a TNF related
CC condition in a cell, tissue, organ or animal (claimed) such as rheumatoid
CC arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology,
CC sickle cell anaemia, diabetes, a cardiovascular disease such as
CC arteriosclerosis, atherosclerosis, restenosis, angina pectoris or
CC myocardial infarction, an infectious disease in a cell such as bacterial,
CC viral, and fungal infections, pneumonia, leprosy and malaria, a malignant
CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
CC lymphoma and multiple myeloma, or a neurological disease such as multiple
CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and
CC Creutzfeldt-Jakob disease
XX
SQ Sequence 108 AA;

Query Match 100.0%; Score 565; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1e-37;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
```

RESULT 2
AAM51173
ID AAM51173 standard; protein; 108 AA.
XX
AC AAM51173;
XX
DT 10-JUN-2002 (first entry)
XX
DE Human Vg/38K-type light chain variable region.
XX
KW Tumour necrosis factor alpha; TNF; antibody; light chain; CDR;
KW complementarity determining region; antirheumatic; antiarthritic;
KW antiulcer; antiasthmatic; antiallergic; antiinflammatory; antisickling;
KW antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;
KW antianginal; cardiant; antibacterial; virucide; fungicide; antileprotic;
KW protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;
KW human; diagnosis; therapy; Vg/38K.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1. .23
FT /label= FR1
FT Region 24. .34
FT /label= CDR1
FT Region 35. .49
FT /label= FR2
FT Region 50. .56
FT /label= CDR2
FT Region 57. .88
FT /label= FR3
FT Region 89. .98
FT /label= CDR3
FT Region 99. .108
FT /label= J3
XX
PN WO200212502-A2.
XX
PD 14-FEB-2002.

XX
PF 07-AUG-2001; 2001WO-US024785.
XX
PR 07-AUG-2000; 2000US-0223360P.
PR 29-SEP-2000; 2000US-0236826P.
PR 01-AUG-2001; 2001US-00920137.
XX
PA (CENZ) CENTOCOR INC.
XX
PI Giles-Komar J, Knight DM, Heavner G, Scallon B, Shealy D;
XX
DR WPI; 2002-217194/27.
DR N-PSDB; ABL53513.
XX
PT Novel isolated mammalian anti-tumor necrosis factor antibody, useful for
PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,
PT angina pectoris, myocardial infarction, leprosy.
XX
PS Example 3; Fig 5; 131pp; English.
XX
CC The present sequence is that of a human Vg/38K-type light chain variable
CC region encoded by a human germline gene in a transgenic mouse used in
CC human monoclonal antibody (mAb) construction. A GenTNV fusion was
CC performed using spleen cells from a hybrid mouse containing human
CC variable and constant region antibody transgenes that was immunised with
CC recombinant human tumour necrosis factor (TNF) alpha. Human mAbs were
CC obtained that bound immobilised human TNF alpha with apparently high
CC avidity. These mAbs had a totally human IgG1, kappa isotype. The mature
CC portion of the light chain variable region of 2 of the mAbs, TNV14 and
CC TNV15, were identical (see AAM51174) to the present sequence, while the
CC light chain variable region of 2 others, TNV148(B) and TNV196 (see
CC AAM51175), differed by a single amino acid residue. The invention
CC provides human, primate, rodent, mammalian, chimeric, humanised and/or
CC complementarity determining region (CDR)-grafted anti-TNF antibodies,
CC immunoglobulins, and cleavage products and variants, as well as anti-TNF
CC antibody compositions, encoding or complementary nucleic acids, vectors,
CC host cells, compositions, formulations, devices, transgenic animals,
CC transgenic plants, and methods of making and using them. The anti-TNF
CC antibody comprises at least a portion of an immunoglobulin molecule,
CC especially the heavy chain and/or light chain variable regions given in
CC the present sequence and in AAM51165, or either all of the CDRs of the
CC heavy chain (see AAM51158-60) or all of the CDRs of the light chain (see
CC AAM51161-63). The antibodies may inhibit TNF-induced cell adhesion
CC molecules, inhibit TNF binding to receptor, or provide Arthritic Index
CC improvement in a mouse model. They are useful for diagnosing or treating
CC a TNF related condition in a cell, tissue, organ or animal (claimed) such
CC as rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis,
CC Crohn's pathology, sickle cell anaemia, diabetes, a cardiovascular
CC disease such as arteriosclerosis, atherosclerosis, restenosis, angina
CC pectoris or myocardial infarction, an infectious disease in a cell such
CC as bacterial, viral, and fungal infections, pneumonia, leprosy and
CC malaria, a malignant disease such as leukaemia, chronic myelocytic
CC leukaemia, Burkitt's lymphoma and multiple myeloma, or a neurological
CC disease such as multiple sclerosis, Parkinson's disease, spinal ataxia,
CC Alzheimer's disease and Creutzfeldt-Jakob disease
XX
SQ Sequence 108 AA;

```
  Query Match             100.0%;  Score 565;  DB 5;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-37;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
```

RESULT 3
AAU76334

ID AAU76334 standard; peptide; 108 AA.
XX
AC AAU76334;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human anti-dual integrin antibody complete variable region #2.
XX
KW Human; antibody; dual integrin; HC CDR; variable region; LC CDR;
KW medical device; immune related disease; rheumatoid arthritis;
KW gastric ulcer; asthma; allergic rhinitis; Crohn's pathology;
KW sickle cell anaemia; diabetes; cardiovascular disease; arteriosclerosis;
KW atherosclerosis; restenosis; angina pectoris; myocardial infarction;
KW infectious disease; pneumonia; leprosy; malaria; malignant disease;
KW leukaemia; chronic myelocytic leukaemia; multiple myeloma;
KW neurological disease; multiple sclerosis; Parkinson's disease;
KW Alzheimer's disease; Creutzfeldt-Jakob disease.
XX
OS Homo sapiens.
XX
PN WO200212501-A2.
XX
PD 14-FEB-2002.
XX
PF 07-AUG-2001; 2001WO-US024784.
XX
PR 07-AUG-2000; 2000US-0223363P.
PR 01-AUG-2001; 2001US-00920267.
XX
PA (CENZ) CENTOCOR INC.
XX
PI Giles-Komar J, Heavner G, Snyder L, Trikha M;
XX
DR WPI; 2002-217193/27.
XX
PT Novel isolated mammalian anti-dual integrin antibody, useful for
PT diagnosing or treating dual integrin related condition such as rheumatoid
PT arthritis, gastric ulcer, asthma, atherosclerosis, restenosis.
XX
PS Claim 1; Page 134; 144pp; English.
XX
CC The invention relates to an isolated mammalian anti-dual integrin
CC antibody having at least one of the human heavy chain or light chain
CC complementary determining region (CDR, HC CDR1-CDR3, LC CDR1-3). Also
CC included are the nucleic acids encoding the CDRs, a vector comprising the
CC nucleic acids, a host cell comprising the vector, an anti-idiotype
CC antibody that binds to the ant-dual integrin, a medical device comprising
CC the antibody suitable for administration by parenteral, subcutaneous,
CC intramuscular, intravenous, intrarticular, intrabronchial,
CC intraabdominal, intracapsular, intracartilaginous, intracavitary,
CC intracelebellar, or other routes as given in specification. The antibody
CC is useful for diagnosing or treating a dual integrin related condition in
CC an animal for example, immune related disease such as rheumatoid
CC arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology,
CC sickle cell anaemia, diabetes, cardiovascular disease such as
CC arteriosclerosis, atherosclerosis, restenosis, angina pectoris,
CC myocardial infarction, infectious disease in a cell such as bacterial,
CC viral, and fungal infections, pneumonia, leprosy, malaria; malignant
CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
CC lymphoma, multiple myeloma; neurological disease such as multiple
CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease,
CC Creutzfeldt-Jakob disease and many other diseases given in the
CC specification. The present sequence is an anti-dual integrin human
CC variable region containing at least one of the six CDRs listed above
CC (AAU76327-AAU76332)
XX
SQ Sequence 108 AA;

```
  Query Match             100.0%;  Score 565;  DB 5;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-37;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108


RESULT 4
ADJ73533
ID   ADJ73533 standard; protein; 108 AA.
XX
AC   ADJ73533;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Erythropoietin light chain mimetibody SeqID 989.
XX
KW   mimetic; CDR mimetibody; gene therapy; transgenic; immune;
KW   cardiovascular; infectious; malignant; neurologic disease; anaemia;
KW   immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
KW   erythropoietin.
XX
OS   Synthetic.
XX
PN   WO2003084477-A2.
XX
PD   16-OCT-2003.
XX
PF   24-MAR-2003; 2003WO-US009139.
XX
PR   29-MAR-2002; 2002US-0368791P.
XX
PA   (CENZ ) CENTOCOR INC.
XX
PI   Heavner GA,  Knight DM,  Scallon BJ,  Ghrayeb J;
XX
DR   WPI; 2003-804237/75.
XX
PT   New CDR mimetibody comprising a portion of a heavy or light chain
PT   variable region comprising human framework or ligand binding region,
PT   useful for preparing a composition for treating e.g., immune,
PT   cardiovascular or neurologic disease.
XX
PS   Example 2; SEQ ID NO 989; 97pp; English.
XX
CC   This invention relates to novel mammalian CDR mimetibodies, specific
CC   portions or variants thereof. Specifically, it refers to an antibody
CC   fragment where a protein has been inserted into, or replaces a portion
CC   of, one or more CDR regions, such that each CDR mimetibody comprises at
CC   least one portion of a heavy chain or light chain variable region, which
CC   itself comprises at least one human framework region and at least one
CC   ligand binding region (LBR). The present invention describes human
CC   mimetibodies, including modified immunoglobulins and cleavage products
CC   that can be useful in gene therapy and the generation of transgenic
CC   plants and animals. Furthermore, the CDR mimetibody is useful for
CC   preparing compositions for modulating, treating or reducing the symptoms
CC   of immune, cardiovascular, infectious, malignant and/ or neurologic
CC   diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
CC   cardiant, antimicrobial, cytostatic and neuroprotective activities. This
CC   polypeptide sequence is an erythropoietin light chain mimetibody of the
CC   invention.
XX
SQ   Sequence 108 AA;

  Query Match             100.0%;  Score 565;  DB 7;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-37;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108


RESULT 5
ADJ73534
ID   ADJ73534 standard; protein; 108 AA.
XX
AC   ADJ73534;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Erythropoietin light chain mimetibody SeqID 990.
XX
KW   mimetic; CDR mimetibody; gene therapy; transgenic; immune;
KW   cardiovascular; infectious; malignant; neurologic disease; anaemia;
KW   immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
KW   erythropoietin.
XX
OS   Synthetic.
XX
PN   WO2003084477-A2.
XX
PD   16-OCT-2003.
XX
PF   24-MAR-2003; 2003WO-US009139.
XX
PR   29-MAR-2002; 2002US-0368791P.
XX
PA   (CENZ ) CENTOCOR INC.
XX
PI   Heavner GA,  Knight DM,  Scallon BJ,  Ghrayeb J;
XX
DR   WPI; 2003-804237/75.
XX
PT   New CDR mimetibody comprising a portion of a heavy or light chain
PT   variable region comprising human framework or ligand binding region,
PT   useful for preparing a composition for treating e.g., immune,
PT   cardiovascular or neurologic disease.
XX
PS   Example 2; SEQ ID NO 990; 97pp; English.
XX
CC   This invention relates to novel mammalian CDR mimetibodies, specific
CC   portions or variants thereof. Specifically, it refers to an antibody
CC   fragment where a protein has been inserted into, or replaces a portion
CC   of, one or more CDR regions, such that each CDR mimetibody comprises at
CC   least one portion of a heavy chain or light chain variable region, which
CC   itself comprises at least one human framework region and at least one
CC   ligand binding region (LBR). The present invention describes human
CC   mimetibodies, including modified immunoglobulins and cleavage products
CC   that can be useful in gene therapy and the generation of transgenic
CC   plants and animals. Furthermore, the CDR mimetibody is useful for
CC   preparing compositions for modulating, treating or reducing the symptoms
CC   of immune, cardiovascular, infectious, malignant and/ or neurologic
CC   diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
CC   cardiant, antimicrobial, cytostatic and neuroprotective activities. This
CC   polypeptide sequence is an erythropoietin light chain mimetibody of the
CC   invention.
XX
SQ   Sequence 108 AA;

  Query Match             100.0%;  Score 565;  DB 7;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-37;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
```

```
RESULT 6
AAM51174
ID   AAM51174 standard; protein; 129 AA.
XX
AC   AAM51174;
XX
DT   10-JUN-2002  (first entry)
XX
DE   Human recombinant mAb TNV14, TNV15 light chain variable region.
XX
KW   Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;
KW   complementarity determining region; antirheumatic; antiarthritic;
KW   antiulcer; antiasthmatic; antiallergic; antiinflammatory; antisickling;
KW   antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;
KW   antianginal; cardiant; antibacterial; virucide; fungicide; antileprotic;
KW   protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;
KW   human; diagnosis; therapy; TNV14; TNV15; monoclonal antibody; mAb.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .20
FT                   /label= Signal_peptide
FT   Protein         20. .129
FT                   /label= Mature_protein
FT   Region          21. .43
FT                   /label= FR1
FT   Region          44. .54
FT                   /label= CDR1
FT   Region          55. .69
FT                   /label= FR2
FT   Region          70. .76
FT                   /label= CDR2
FT   Region          77. .108
FT                   /label= FR3
FT   Region          109. .118
FT                   /label= CDR3
FT   Region          119. .129
FT                   /label= J3
XX
PN   WO200212502-A2.
XX
PD   14-FEB-2002.
XX
PF   07-AUG-2001; 2001WO-US024785.
XX
PR   07-AUG-2000; 2000US-0223360P.
PR   29-SEP-2000; 2000US-0236826P.
PR   01-AUG-2001; 2001US-00920137.
XX
PA   (CENZ ) CENTOCOR INC.
XX
PI   Giles-Komar J,  Knight DM,  Heavner G,  Scallon B,  Shealy D;
XX
DR   WPI; 2002-217194/27.
DR   N-PSDB; ABL53514.
XX
PT   Novel isolated mammalian anti-tumor necrosis factor antibody, useful for
PT   treating sickle cell anemia, diabetes, atherosclerosis, restenosis,
PT   angina pectoris, myocardial infarction, leprosy.
XX
PS   Example 3; Fig 5; 131pp; English.
XX
CC   The present sequence is that of the light chain variable region of anti-
CC   tumour necrosis factor (TNF) human recombinant monoclonal antibodies
CC   (mAbs) TNV14 and TNV15. These are human mAbs produced from a GenTNV
CC   fusion using spleen cells from a hybrid mouse containing human variable
CC   and constant region antibody transgenes that was immunised with human TNF
CC   alpha. The human mAbs bind immobilised human TNF alpha with high avidity
CC   and have a totally human IgG1, kappa isotype. The mature portion of the
CC   light chain variable region is identical to that of the Vg/38-type light
CC   chain germline sequence (see AAM51173). The light chain variable regions
CC   of 2 other human mAbs (see AAM51175) show a single amino acid difference.
CC   The invention provides human, primate, mammalian, rodent, chimeric,
CC   humanised and/or complementarity determining region (CDR)-grafted anti-
CC   TNF antibodies, immunoglobulins, cleavage products and other specified
CC   portions and variants, as well as anti-TNF antibody compositions,
CC   encoding or complementary nucleic acids, vectors, host cells,
CC   compositions, formulations, devices, transgenic animals, transgenic
CC   plants, and methods of making and using them. The anti-TNF antibody
CC   comprises at least a portion of an immunoglobulin molecule, especially
CC   the heavy chain and/or light chain variable regions given in the present
CC   sequence and in AAM51165, or either all of the CDRs of the heavy chain
CC   (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-
CC   63). The antibodies may inhibit TNF-induced cell adhesion molecules,
CC   inhibit TNF binding to receptor, or provide Arthritic Index improvement
CC   in a mouse model. They are useful for diagnosing or treating a TNF
CC   related condition in a cell, tissue, organ or animal (claimed) such as
CC   rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's
CC   pathology, sickle cell anaemia, diabetes, a cardiovascular disease such
CC   as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or
CC   myocardial infarction, an infectious disease in a cell such as bacterial,
CC   viral, and fungal infections, pneumonia, leprosy and malaria, a malignant
CC   disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
CC   lymphoma and multiple myeloma, or a neurological disease such as multiple
CC   sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and
CC   Creutzfeldt-Jakob disease
XX
SQ   Sequence 129 AA;

  Query Match             100.0%;  Score 565;  DB 5;  Length 129;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-37;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 128


RESULT 7
AAM51175
ID   AAM51175 standard; protein; 129 AA.
XX
AC   AAM51175;
XX
DT   10-JUN-2002  (first entry)
XX
DE   Human mAb TNV148(B), TNV196 light chain variable region.
XX
KW   Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;
KW   complementarity determining region; antirheumatic; antiarthritic;
KW   antiulcer; antiasthmatic; antiallergic; antiinflammatory; antisickling;
KW   antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;
KW   antianginal; cardiant; antibacterial; virucide; fungicide; antileprotic;
KW   protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;
KW   human; diagnosis; therapy; TNV148(B); TNV196; monoclonal antibody; mAb.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .20
FT                   /label= Signal_peptide
FT   Protein         20. .129
FT                   /label= Mature_protein
FT   Region          21. .43
FT                   /label= FR1
FT   Region          44. .54
FT                   /label= CDR1
FT   Region          55. .69
FT                   /label= FR2
```

```
FT   Region          70. .76
FT                   /label= CDR2
FT   Region          77. .108
FT                   /label= FR3
FT   Region          109. .118
FT                   /label= CDR3
FT   Region          119. .129
FT                   /label= J3
XX
PN   WO200212502-A2.
XX
PD   14-FEB-2002.
XX
PF   07-AUG-2001; 2001WO-US024785.
XX
PR   07-AUG-2000; 2000US-0223360P.
PR   29-SEP-2000; 2000US-0236826P.
PR   01-AUG-2001; 2001US-00920137.
XX
PA   (CENZ ) CENTOCOR INC.
XX
PI   Giles-Komar J,  Knight DM,  Heavner G,  Scallon B,  Shealy D;
XX
DR   WPI; 2002-217194/27.
DR   N-PSDB; ABL53515.
XX
PT   Novel isolated mammalian anti-tumor necrosis factor antibody, useful for
PT   treating sickle cell anemia, diabetes, atherosclerosis, restenosis,
PT   angina pectoris, myocardial infarction, leprosy.
XX
PS   Example 3; Fig 5; 131pp; English.
XX
CC   The present sequence is that of the light chain variable region of anti-
CC   tumour necrosis factor (TNF) human recombinant monoclonal antibodies
CC   (mAbs) TNV148(B) and TNV196. These are human mAbs produced from a GenTNV
CC   fusion using spleen cells from a hybrid mouse containing human variable
CC   and constant region antibody transgenes that was immunised with human TNF
CC   alpha. The human mAbs bind immobilised human TNF alpha with high avidity
CC   and have a totally human IgG1, kappa isotype. The mature portion of the
CC   light chain variable region differs from that of the Vg/38-type light
CC   chain germline sequence (see AAM51173) by a single residue (Tyr-50
CC   replacing Ser). The light chain variable regions of 2 other human mAbs
CC   (see AAM51174) were identical to the germline sequence. The invention
CC   provides isolated human, primate, rodent, mammalian, chimeric, humanised
CC   and/or complementarity determining region (CDR)-grafted anti-TNF
CC   antibodies, immunoglobulins, cleavage products and other specified
CC   portions and variants, as well as anti-TNF antibody compositions,
CC   encoding or complementary nucleic acids, vectors, host cells,
CC   compositions, formulations, devices, transgenic animals, transgenic
CC   plants, and methods of making and using them. The anti-TNF antibody
CC   comprises at least a portion of an immunoglobulin molecule, especially
CC   the heavy chain and/or light chain variable regions given in the present
CC   sequence and in AAM51165, or either all of the CDRs of the heavy chain
CC   (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-
CC   63). The antibodies may inhibit TNF-induced cell adhesion molecules,
CC   inhibit TNF binding to receptor, or provide Arthritic Index improvement
CC   in a mouse model. They are useful for diagnosing or treating a TNF
CC   related condition in a cell, tissue, organ or animal (claimed) such as
CC   rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's
CC   pathology, sickle cell anaemia, diabetes, a cardiovascular disease such
CC   as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or
CC   myocardial infarction, an infectious disease in a cell such as bacterial,
CC   viral, and fungal infections, pneumonia, leprosy and malaria, a malignant
CC   disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
CC   lymphoma and multiple myeloma, or a neurological disease such as multiple
CC   sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and
CC   Creutzfeldt-Jakob disease
XX
SQ   Sequence 129 AA;

  Query Match             100.0%;  Score 565;  DB 5;  Length 129;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-37;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 128


RESULT 8
AAB72884
ID   AAB72884 standard; protein; 108 AA.
XX
AC   AAB72884;
XX
DT   10-MAY-2001  (first entry)
XX
DE   Human anti-HER2/neu antibody 2-E8 light chain.
XX
KW   Human; HER2; neu; erbB2; oncogene; cancer; antibody; immunotherapy; 3-F2;
KW   1-D2; 2-E8; growth factor receptor.
XX
OS   Homo sapiens.
XX
PN   WO200109187-A2.
XX
PD   08-FEB-2001.
XX
PF   25-JUL-2000; 2000WO-US020272.
XX
PR   29-JUL-1999;   99US-0146313P.
PR   10-MAR-2000; 2000US-0188539P.
XX
PA   (MEDA-) MEDAREX INC.
XX
PI   Keler T,  Deo Y;
XX
DR   WPI; 2001-168698/17.
DR   N-PSDB; AAF75590.
XX
PT   New human monoclonal antibody that specifically binds to growth factor
PT   receptor HER2/neu, for treating, preventing or diagnosing diseases
PT   characterized by aberrant HER2/neu expression e.g. cancers.
XX
PS   Disclosure; Page 110; 113pp; English.
XX
CC   The present invention provides the protein and coding sequences for human
CC   monoclonal antibodies which bind specifically to the HER2/neu growth
CC   factor receptor (also known as erbB2). These are designated 3-F2, 1-D2
CC   and 2-E8. They can be used in the immunotherapy-based treatment and
CC   prognosis of cancers, particularly adenocarcinomas such as salivary
CC   gland, stomach, kidney, mammary gland, lung and squamous cell carcinomas,
CC   and ovarian cancer. The present sequence is part of an antibody of the
CC   invention
XX
SQ   Sequence 108 AA;

  Query Match             96.8%;  Score 547;  DB 4;  Length 108;
  Best Local Similarity   96.3%;  Pred. No. 2.9e-36;
  Matches  104;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||:||| |||::||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPYTFGQGTKLEIK 108


RESULT 9
ADF11411
```

```
ID   ADF11411 standard; protein; 109 AA.
XX
AC   ADF11411;
XX
DT   12-FEB-2004  (first entry)
XX
DE   16E1 anti-OPGL antibody kappa chain variable region SEQ ID NO:24.
XX
KW   human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
KW   osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
KW   osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.
XX
OS   Homo sapiens.
XX
PN   WO2003086289-A2.
XX
PD   23-OCT-2003.
XX
PF   07-APR-2003; 2003WO-US010749.
XX
PR   05-APR-2002; 2002US-0370407P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boyle WJ,  Medlock E,  Sullivan JK,  Elliott RL,  Martin F,  Huang H;
XX
DR   WPI; 2003-845253/78.
DR   N-PSDB; ADF11410.
XX
PT   New isolated antibody that specifically binds osteoprotegerin ligand,
PT   useful for diagnosing or treating bone disorders, such as osteoporosis,
PT   bone loss from arthritis, Paget's disease or osteopenia.
XX
PS   Claim 6; SEQ ID NO 24; 156pp; English.
XX
CC   The present invention describes an isolated human antibody (I) that
CC   specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
CC   pharmaceutical composition comprising a pharmaceutical carrier and a
CC   therapeutic amount of (I); (2) methods of treating an osteopenic disorder
CC   in a patient, comprising administering to a patient the pharmaceutical
CC   composition of (1) or a pharmaceutical amount of (I); and (3) a method
CC   for detecting OPGL in a biological sample, comprising contacting the
CC   sample with (I) under conditions that allow for binding of the antibody
CC   to OPGL, and measuring the level of bound antibody in the sample. (I) has
CC   osteopathic, antiarthritic and cytostatic activities, and can be used in
CC   gene therapy. The composition and methods are useful in diagnosing or
CC   treating bone disorders, such as osteoporosis, bone loss from arthritis,
CC   Paget's disease or osteopenia. The antibody (I) may also be used for
CC   detecting OPGL in biological samples and in identifying cells or tissues
CC   that produce the protein. The present sequence represents a sequence
CC   which is used in the exemplification of the present invention.
XX
SQ   Sequence 109 AA;

  Query Match             96.8%;  Score 547;  DB 7;  Length 109;
  Best Local Similarity   96.3%;  Pred. No. 2.9e-36;
  Matches  104;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||||:||| |||::||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPYTFGQGTKLEIK 108


RESULT 10
ADF11435
ID   ADF11435 standard; protein; 215 AA.
XX
AC   ADF11435;
XX
DT   12-FEB-2004  (first entry)
XX
DE   16E1 anti-OPGL antibody light chain SEQ ID NO:48.
XX
KW   human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
KW   osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
KW   osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.
XX
OS   Homo sapiens.
XX
PN   WO2003086289-A2.
XX
PD   23-OCT-2003.
XX
PF   07-APR-2003; 2003WO-US010749.
XX
PR   05-APR-2002; 2002US-0370407P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boyle WJ,  Medlock E,  Sullivan JK,  Elliott RL,  Martin F,  Huang H;
XX
DR   WPI; 2003-845253/78.
DR   N-PSDB; ADF11434.
XX
PT   New isolated antibody that specifically binds osteoprotegerin ligand,
PT   useful for diagnosing or treating bone disorders, such as osteoporosis,
PT   bone loss from arthritis, Paget's disease or osteopenia.
XX
PS   Claim 16; SEQ ID NO 48; 156pp; English.
XX
CC   The present invention describes an isolated human antibody (I) that
CC   specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
CC   pharmaceutical composition comprising a pharmaceutical carrier and a
CC   therapeutic amount of (I); (2) methods of treating an osteopenic disorder
CC   in a patient, comprising administering to a patient the pharmaceutical
CC   composition of (1) or a pharmaceutical amount of (I); and (3) a method
CC   for detecting OPGL in a biological sample, comprising contacting the
CC   sample with (I) under conditions that allow for binding of the antibody
CC   to OPGL, and measuring the level of bound antibody in the sample. (I) has
CC   osteopathic, antiarthritic and cytostatic activities, and can be used in
CC   gene therapy. The composition and methods are useful in diagnosing or
CC   treating bone disorders, such as osteoporosis, bone loss from arthritis,
CC   Paget's disease or osteopenia. The antibody (I) may also be used for
CC   detecting OPGL in biological samples and in identifying cells or tissues
CC   that produce the protein. The present sequence represents a sequence
CC   which is used in the exemplification of the present invention.
XX
SQ   Sequence 215 AA;

  Query Match             96.8%;  Score 547;  DB 7;  Length 215;
  Best Local Similarity   96.3%;  Pred. No. 5.6e-36;
  Matches  104;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||||:||| |||::||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPYTFGQGTKLEIK 108


RESULT 11
ADM41547
ID   ADM41547 standard; protein; 128 AA.
XX
AC   ADM41547;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Anti-interleukin-1 receptor type 1 antibody kappa chain variable region.
XX
```

```
KW   Human; monoclonal antibody; antibody; interleukin-1; receptor;
KW   antiasthmatic; antiinflammatory; dermatological; antiallergic;
KW   protozoacide; antirheumatic; antiarthritic; osteopathic; vasotropic;
KW   analgesic; antidiabetic; nephrotropic; antianaemic; nootropic;
KW   anticonvulsant; dermatological; antigout; antiparkinsonian; antidiabetic;
KW   cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO2004022718-A2.
XX
PD   18-MAR-2004.
XX
PF   05-SEP-2003; 2003WO-US027978.
XX
PR   06-SEP-2002; 2002US-0408719P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Varnum B,  Vezina C,  Witte A,  Qian X,  Martin F,  Huang H;
PI   Elliott G;
XX
DR   WPI; 2004-248462/23.
DR   N-PSDB; ADM41546.
XX
PT   Isolated human antibody that specifically binds interleukin-1 receptor
PT   type 1 (IL-1R1) useful for treating IL-1 mediated diseases such as
PT   rheumatoid arthritis, osteoarthritis and inflammatory conditions.
XX
PS   Claim 2; SEQ ID NO 12; 179pp; English.
XX
CC   The present sequence is that of human anti-interleukin-1 receptor type 1
CC   (IL-1R1) monoclonal antibody (MAb) 26F5 kappa chain variable region.
CC   Human MAbs to IL-1R1 were prepared using the HCo7 strain of transgenic
CC   mice, which expresses human antibody genes. These mice were immunised
CC   with purified recombinant IL-1R1, and splenocytes from immunised mice
CC   were fused to a mouse myeloma cell line to generate hybridomas.
CC   Hybridomas which secreted a MAb that bound with high avidity to IL-1R1
CC   were selected. The MAbs inhibit IL-1 signalling by competing with IL-
CC   1beta and IL-1alpha binding to IL-1R. These MAbs, as well as single chain
CC   antibodies single chain Fv antibodies, Fab antibodies, Fab' antibodies
CC   and (Fab')2 antibodies derived from them, are used in methods of treating
CC   IL-1 mediated diseases or for detecting the amount of IL-1R1 in a sample.
CC   IL-1 mediated diseases include acute pancreatitis, amyotrophic lateral
CC   sclerosis, Alzheimer's disease, cachexia, anorexia, asthma,
CC   atherosclerosis, autoimmune vasculitis, chronic fatigue syndrome,
CC   Clostridium associated illnesses, coronary conditions, cancer including
CC   leukaemia and tumour metastasis, diabetes, endometriosis, fever,
CC   fibromyalgia, glomerulonephritis, graft versus host disease,
CC   osteoarthritis, rheumatoid arthritis, inflammatory eye disease,
CC   ischaemia, Kawasaki's disease, learning impairment, lung diseases,
CC   multiple sclerosis, myopathy, osteoporosis, pain, Parkinson's disease,
CC   periodontal disease, pre-term labour, psoriasis, reperfusion injury,
CC   septic shock, side effects of radiation therapy, temporal mandibular
CC   joint disease, sleep disturbance, uveitis, or an inflammatory condition
CC   resulting from strain, sprain, cartilage damage, trauma, orthopaedic
CC   surgery, infection or other disease processes.
XX
SQ   Sequence 128 AA;

  Query Match             96.6%;  Score 546;  DB 8;  Length 128;
  Best Local Similarity   97.2%;  Pred. No. 4.1e-36;
  Matches  105;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||||| ||| ||||:||
Db         81 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPLTFGGGTKVEIK 128
```

```
RESULT 12
ADD89877
ID   ADD89877 standard; protein; 130 AA.
XX
AC   ADD89877;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human anti-TNF antibody 9E7 light chain variable region.
XX
KW   Human; Tumour necrosis factor; TNF; antibody; cytostatic; anabolic;
KW   eating-disorders-gen; immunomodulator; antimicrobial; cardiovascular-gen;
KW   neuroprotective.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          44. .54
FT                   /note= "CDR1"
FT   Region          65. .71
FT                   /note= "CDR2"
FT   Region          109. .118
FT                   /note= "CDR3"
XX
PN   WO2003083061-A2.
XX
PD   09-OCT-2003.
XX
PF   24-MAR-2003; 2003WO-US009072.
XX
PR   26-MAR-2002; 2002US-0367903P.
XX
PA   (CENZ ) CENTOCOR INC.
XX
PI   Giles-Komar J,  Scallon BJ,  Carton JM;
XX
DR   WPI; 2003-804040/75.
DR   N-PSDB; ADD89883.
XX
PT   New isolated mammalian anti-tumor necrosis factor (TNF) antibody, useful
PT   for diagnosing or treating an anti-TNF related condition, e.g. cancer,
PT   anorexia, cachexia, or bacterial infection.
XX
PS   Claim 1; Fig 3B; 87pp; English.
XX
CC   The present sequence is that of the light chain variable region of human
CC   anti-tumour necrosis factor (TNF) monoclonal antibody 9E7. This human TNF
CC   reactive IgG monoclonal antibody was generated by cloning variable and
CC   constant region DNA in vector pC4 and expression in CHO cells. The
CC   invention provides isolated human, primate, rodent, mammalian, chimeric,
CC   humanized and/or CDR-grafted anti-TNF antibodies, immunoglobulins, their
CC   cleavage products, other specified portions and variants, as well as anti
CC   -TNF antibody compositions, nucleic acids encoding these, vectors, host
CC   cells, methods for producing the antibodies using a host cell, transgenic
CC   animal or transgenic plant or plant cell, and therapeutic compositions,
CC   methods and devices. The antibody, nucleic acid, protein, composition and
CC   methods are useful for diagnosing or treating an anti-TNF related
CC   condition, e.g. cancer, anorexia, cachexia, or an immune, cardiovascular,
CC   infectious, and/or neurological disease.
XX
SQ   Sequence 130 AA;

  Query Match             96.6%;  Score 546;  DB 7;  Length 130;
  Best Local Similarity   97.2%;  Pred. No. 4.2e-36;
  Matches  105;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||||| ||| ||||:||
Db         81 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPLTFGGGTKVEIK 128
```

```
RESULT 13
ADS64664
ID   ADS64664 standard; protein; 130 AA.
XX
AC   ADS64664;
XX
DT   16-DEC-2004  (first entry)
XX
DE   Human 9E7LC light chain protein.
XX
KW   Tumour necrosis factor; TNF; immunotherapy; TNF related diseases;
KW   obesity; immune related disease; rheumatoid arthritis;
KW   cardiovascular disease; stroke; malignant disease; leukaemia;
KW   neurological disease; multiple sclerosis; infection; hepatitis;
KW   anorectic; antiarthritic; cerebroprotective; vasotropic; cytostatic;
KW   neuroprotective; antibacterial; antiinflammatory; hepatotropic; virucide;
KW   human; 9E7LC; light chain.
XX
OS   Homo sapiens.
XX
PN   US2004185047-A1.
XX
PD   23-SEP-2004.
XX
PF   21-MAR-2003; 2003US-00394471.
XX
PR   21-MAR-2003; 2003US-00394471.
XX
PA   (GILE/) GILES-KOMAR J.
PA   (SCAL/) SCALLON B J.
PA   (CART/) CARTON J M.
XX
PI   Giles-Komar J,  Scallon BJ,  Carton JM;
XX
DR   WPI; 2004-676151/66.
DR   N-PSDB; ADS64661.
XX
PT   Novel isolated mammalian anti-tumor necrosis factor (TNF) alpha antibody
PT   capable of inhibiting binding of TNF alpha to TNF receptor, useful for
PT   treating TNF-related diseases such as obesity or rheumatoid arthritis.
XX
PS   Example 4; Fig 3; 45pp; English.
XX
CC   The present invention relates to a mammalian anti-tumour necrosis factor
CC   (TNF) antibody capable of inhibiting binding of TNF alpha to TNF
CC   receptor. The invention is useful for diagnosing or treating an anti-TNF
CC   related condition in a cell, tissue, organ or animal and in
CC   immunotherapy. The invention is also useful for treating TNF related
CC   diseases chosen from obesity, immune related disease such as rheumatoid
CC   arthritis, cardiovascular disease such as stroke, malignant disease such
CC   as leukaemia, neurological disease such as multiple sclerosis and
CC   bacterial or viral infections such as hepatitis. The present sequence is
CC   the human 9E7LC light chain protein (variable region and J-region). This
CC   sequence is used in the exemplification of the invention.
XX
SQ   Sequence 130 AA;

  Query Match             96.6%;  Score 546;  DB 8;  Length 130;
  Best Local Similarity   97.2%;  Pred. No. 4.2e-36;
  Matches  105;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||| ||| ||||:||
Db         81 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPLTFGGGTKVEIK 128


RESULT 14
```

```
ADS64653
ID   ADS64653 standard; protein; 130 AA.
XX
AC   ADS64653;
XX
DT   16-DEC-2004  (first entry)
XX
DE   Human anti-TNF antibody light chain variable region protein #2.
XX
KW   Tumour necrosis factor; TNF; immunotherapy; TNF related diseases;
KW   obesity; immune related disease; rheumatoid arthritis;
KW   cardiovascular disease; stroke; malignant disease; leukaemia;
KW   neurological disease; multiple sclerosis; infection; hepatitis;
KW   anorectic; antiarthritic; cerebroprotective; vasotropic; cytostatic;
KW   neuroprotective; antibacterial; antiinflammatory; hepatotropic; virucide;
KW   anti-TNF antibody; human; light chain.
XX
OS   Homo sapiens.
XX
PN   US2004185047-A1.
XX
PD   23-SEP-2004.
XX
PF   21-MAR-2003; 2003US-00394471.
XX
PR   21-MAR-2003; 2003US-00394471.
XX
PA   (GILE/) GILES-KOMAR J.
PA   (SCAL/) SCALLON B J.
PA   (CART/) CARTON J M.
XX
PI   Giles-Komar J,  Scallon BJ,  Carton JM;
XX
DR   WPI; 2004-676151/66.
XX
PT   Novel isolated mammalian anti-tumor necrosis factor (TNF) alpha antibody
PT   capable of inhibiting binding of TNF alpha to TNF receptor, useful for
PT   treating TNF-related diseases such as obesity or rheumatoid arthritis.
XX
PS   Claim 1; SEQ ID NO 16; 45pp; English.
XX
CC   The present invention relates to a mammalian anti-tumour necrosis factor
CC   (TNF) antibody capable of inhibiting binding of TNF alpha to TNF
CC   receptor. The invention is useful for diagnosing or treating an anti-TNF
CC   related condition in a cell, tissue, organ or animal and in
CC   immunotherapy. The invention is also useful for treating TNF related
CC   diseases chosen from obesity, immune related disease such as rheumatoid
CC   arthritis, cardiovascular disease such as stroke, malignant disease such
CC   as leukaemia, neurological disease such as multiple sclerosis and
CC   bacterial or viral infections such as hepatitis. The present sequence is
CC   the human anti-TNF antibody light chain variable region protein.
XX
SQ   Sequence 130 AA;

  Query Match             96.6%;  Score 546;  DB 8;  Length 130;
  Best Local Similarity   97.2%;  Pred. No. 4.2e-36;
  Matches  105;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||| ||| ||||:||
Db         81 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPLTFGGGTKVEIK 128


RESULT 15
ADM41573
ID   ADM41573 standard; protein; 235 AA.
XX
AC   ADM41573;
XX
```

DT 03-JUN-2004 (first entry)
XX
DE Anti-interleukin-1 receptor type 1 antibody light chain.
XX
KW Human; monoclonal antibody; antibody; interleukin-1; receptor;
KW antiasthmatic; antiinflammatory; dermatological; antiallergic;
KW protozoacide; antirheumatic; antiarthritic; osteopathic; vasotropic;
KW analgesic; antidiabetic; nephrotropic; antianaemic; nootropic;
KW anticonvulsant; dermatological; antigout; antiparkinsonian; antidiabetic;
KW cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004022718-A2.
XX
PD 18-MAR-2004.
XX
PF 05-SEP-2003; 2003WO-US027978.
XX
PR 06-SEP-2002; 2002US-0408719P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Varnum B, Vezina C, Witte A, Qian X, Martin F, Huang H;
PI Elliott G;
XX
DR WPI; 2004-248462/23.
DR N-PSDB; ADM41572.
XX
PT Isolated human antibody that specifically binds interleukin-1 receptor
PT type 1 (IL-1R1) useful for treating IL-1 mediated diseases such as
PT rheumatoid arthritis, osteoarthritis and inflammatory conditions.
XX
PS Claim 4; SEQ ID NO 38; 179pp; English.
XX
CC The present sequence is that of a human anti-interleukin-1 receptor type
CC 1 (IL-1R1) monoclonal antibody (MAb) light chain. The invention provides
CC antibodies that comprise this sequence. Human MAbs to IL-1R1 were
CC prepared using the HCo7 strain of transgenic mice, which expresses human
CC antibody genes. These mice were immunised with purified recombinant IL-
CC 1R1, and splenocytes from immunised mice were fused to a mouse myeloma
CC cell line to generate hybridomas. Hybridomas which secreted a MAb that
CC bound with high avidity to IL-1R1 were selected. The MAbs inhibit IL-1
CC signalling by competing with IL-1beta and IL-1alpha binding to IL-1R.
CC These MAbs, as well as single chain antibodies single chain Fv
CC antibodies, Fab antibodies, Fab' antibodies and (Fab')2 antibodies
CC derived from them, are used in methods of treating IL-1 mediated diseases
CC or for detecting the amount of IL-1R1 in a sample. IL-1 mediated diseases
CC include acute pancreatitis, amyotrophic lateral sclerosis, Alzheimer's
CC disease, cachexia, anorexia, asthma, atherosclerosis, autoimmune
CC vasculitis, chronic fatigue syndrome, Clostridium associated illnesses,
CC coronary conditions, cancer including leukaemia and tumour metastasis,
CC diabetes, endometriosis, fever, fibromyalgia, glomerulonephritis, graft
CC versus host disease, osteoarthritis, rheumatoid arthritis, inflammatory
CC eye disease, ischaemia, Kawasaki's disease, learning impairment, lung
CC diseases, multiple sclerosis, myopathy, osteoporosis, pain, Parkinson's
CC disease, periodontal disease, pre-term labour, psoriasis, reperfusion
CC injury, septic shock, side effects of radiation therapy, temporal
CC mandibular joint disease, sleep disturbance, uveitis, or an inflammatory
CC condition resulting from strain, sprain, cartilage damage, trauma,
CC orthopaedic surgery, infection or other disease processes.
XX
SQ Sequence 235 AA;

Query Match 96.6%; Score 546; DB 8; Length 235;
Best Local Similarity 97.2%; Pred. No. 7.3e-36;
Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80

Qy 61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
Db 81 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPLTFGGGTKVEIK 128

RESULT 16
ADS19298
ID ADS19298 standard; protein; 108 AA.
XX
AC ADS19298;
XX
DT 18-NOV-2004 (first entry)
XX
DE Light chain variable region of human mAb 3G6 antibody protein SeqID 9.
XX
KW human; antibody; mAb 3G6; lymphocyte migration;
KW inflammatory bowel disease; Crohn's disease; gastroenteritis;
KW pulmonary inflammatory disease; asthma; chronic bronchitis;
KW graft rejection; psoriasis; eczema; urticaria; scleroderma;
KW autoimmune disease; multiple sclerosis; diabetes; glomerulonephritis;
KW autoimmune thyroiditis; Behcet's syndrome; viral infection; cancer;
KW neoplastic disease; leukaemia; lymphoma; antiinflammatory; antiasthmatic;
KW immunosuppressive; antipsoriatic; dermatological; neuroprotective;
KW antidiabetic; nephrotropic; virucide; cytostatic; vasotropic;
KW alphaE integrin; CD103; alphaE-beta7.
XX
OS Homo sapiens.
XX
PN US2003232387-A1.
XX
PD 18-DEC-2003.
XX
PF 14-JUN-2002; 2002US-00173551.
XX
PR 14-JUN-2002; 2002US-00173551.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Lu C;
XX
DR WPI; 2004-178738/17.
DR N-PSDB; ADS19297.
XX
PT Novel antibody which binds activated alpha-E integrin, specifically to
PT activation-induced epitope on integrin alpha-E chain (CD103), useful for
PT treating inflammatory bowel diseases e.g., Crohn's disease,
PT gastroenteritis.
XX
PS Disclosure; SEQ ID NO 9; 67pp; English.
XX
CC This invention relates to novel antibody and antigen-binding fragments of
CC antibodies that bind alphaE-beta7 integrin chains (CD103). Specifically,
CC it refers to the binding of activation induced epitopes present on
CC activated alphaE integrins, where these integrins are activated by
CC exposure to divalent cations (e.g. Mn2+), to phorbol esters or suitable
CC growth factors and/ or mitogens. The present invention describes the
CC alphaE-beta7 integrin as a homing receptor that mediates lymphocyte
CC migration to mucosal epithelium. As such, compositions of this invention
CC are useful for treating a subject having an inflammatory bowel disease
CC such as Crohn's disease or gastroenteritis or pulmonary inflammatory
CC diseases such as asthma and chronic bronchitis. Furthermore, such
CC compositions can be used for inhibiting graft rejection, psoriasis,
CC eczema, urticaria, scleroderma, autoimmune diseases such as multiple
CC sclerosis, diabetes, glomerulonephritis, autoimmune thyroiditis, Behcet's
CC syndrome, viral infections, cancer and/or neoplastic diseases such as
CC leukaemias and lymphomas. Accordingly, they exhibit antiinflammatory,
CC antiasthmatic, immunosuppressive, antipsoriatic, dermatological,
CC neuroprotective, antidiabetic, nephrotropic, virucide, cytostatic and
CC vasotropic activities. This polypeptide sequence is a human antibody that
CC binds the integrin alphaE chain of the invention.
XX
SQ Sequence 108 AA;

Query Match 96.3%; Score 544; DB 8; Length 108;

```
  Best Local Similarity   97.2%;  Pred. No. 5e-36;
  Matches  105;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||||| ||| ||||:||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPGTFGQGTKVEIK 108


RESULT 17
ADF11395
ID   ADF11395 standard; protein; 109 AA.
XX
AC   ADF11395;
XX
DT   12-FEB-2004  (first entry)
XX
DE   22B3 anti-OPGL antibody kappa chain variable region SEQ ID NO:8.
XX
KW   human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
KW   osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
KW   osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.
XX
OS   Homo sapiens.
XX
PN   WO2003086289-A2.
XX
PD   23-OCT-2003.
XX
PF   07-APR-2003; 2003WO-US010749.
XX
PR   05-APR-2002; 2002US-0370407P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boyle WJ,  Medlock E,  Sullivan JK,  Elliott RL,  Martin F,  Huang H;
XX
DR   WPI; 2003-845253/78.
DR   N-PSDB; ADF11394.
XX
PT   New isolated antibody that specifically binds osteoprotegerin ligand,
PT   useful for diagnosing or treating bone disorders, such as osteoporosis,
PT   bone loss from arthritis, Paget's disease or osteopenia.
XX
PS   Claim 6; SEQ ID NO 8; 156pp; English.
XX
CC   The present invention describes an isolated human antibody (I) that
CC   specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
CC   pharmaceutical composition comprising a pharmaceutical carrier and a
CC   therapeutic amount of (I); (2) methods of treating an osteopenic disorder
CC   in a patient, comprising administering to a patient the pharmaceutical
CC   composition of (1) or a pharmaceutical amount of (I); and (3) a method
CC   for detecting OPGL in a biological sample, comprising contacting the
CC   sample with (I) under conditions that allow for binding of the antibody
CC   to OPGL, and measuring the level of bound antibody in the sample. (I) has
CC   osteopathic, antiarthritic and cytostatic activities, and can be used in
CC   gene therapy. The composition and methods are useful in diagnosing or
CC   treating bone disorders, such as osteoporosis, bone loss from arthritis,
CC   Paget's disease or osteopenia. The antibody (I) may also be used for
CC   detecting OPGL in biological samples and in identifying cells or tissues
CC   that produce the protein. The present sequence represents a sequence
CC   which is used in the exemplification of the present invention.
XX
SQ   Sequence 109 AA;

  Query Match             95.9%;  Score 542;  DB 7;  Length 109;
  Best Local Similarity   94.4%;  Pred. No. 7.3e-36;
  Matches  102;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||:|||||:||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVNSYLAWFQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||:|||||:|||||||||||||||| |||::||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAIYYCQQRSNWPPFTFGQGTKLEIK 108


RESULT 18
ADF11419
ID   ADF11419 standard; protein; 215 AA.
XX
AC   ADF11419;
XX
DT   12-FEB-2004  (first entry)
XX
DE   22B3 anti-OPGL antibody light chain SEQ ID NO:32.
XX
KW   human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
KW   osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
KW   osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.
XX
OS   Homo sapiens.
XX
PN   WO2003086289-A2.
XX
PD   23-OCT-2003.
XX
PF   07-APR-2003; 2003WO-US010749.
XX
PR   05-APR-2002; 2002US-0370407P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boyle WJ,  Medlock E,  Sullivan JK,  Elliott RL,  Martin F,  Huang H;
XX
DR   WPI; 2003-845253/78.
DR   N-PSDB; ADF11418.
XX
PT   New isolated antibody that specifically binds osteoprotegerin ligand,
PT   useful for diagnosing or treating bone disorders, such as osteoporosis,
PT   bone loss from arthritis, Paget's disease or osteopenia.
XX
PS   Claim 16; SEQ ID NO 32; 156pp; English.
XX
CC   The present invention describes an isolated human antibody (I) that
CC   specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
CC   pharmaceutical composition comprising a pharmaceutical carrier and a
CC   therapeutic amount of (I); (2) methods of treating an osteopenic disorder
CC   in a patient, comprising administering to a patient the pharmaceutical
CC   composition of (1) or a pharmaceutical amount of (I); and (3) a method
CC   for detecting OPGL in a biological sample, comprising contacting the
CC   sample with (I) under conditions that allow for binding of the antibody
CC   to OPGL, and measuring the level of bound antibody in the sample. (I) has
CC   osteopathic, antiarthritic and cytostatic activities, and can be used in
CC   gene therapy. The composition and methods are useful in diagnosing or
CC   treating bone disorders, such as osteoporosis, bone loss from arthritis,
CC   Paget's disease or osteopenia. The antibody (I) may also be used for
CC   detecting OPGL in biological samples and in identifying cells or tissues
CC   that produce the protein. The present sequence represents a sequence
CC   which is used in the exemplification of the present invention.
XX
SQ   Sequence 215 AA;

  Query Match             95.9%;  Score 542;  DB 7;  Length 215;
  Best Local Similarity   94.4%;  Pred. No. 1.4e-35;
  Matches  102;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||:|||||:||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVNSYLAWFQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
```

```
                    ||||||||||||||||||||||||:|||||||||||||||| |||::||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAIYYCQQRSNWPPFTFGQGTKLEIK 108
```

RESULT 19
ADI22138
ID ADI22138 standard; protein; 108 AA.
XX
AC ADI22138;
XX
DT 22-APR-2004 (first entry)
XX
DE Anti-platelet autoantibody related light chain amino acid L76 SEQ:101.
XX
KW anti-platelet autoantibody; autoantibody; blood clotting inhibition;
KW thrombus; platelet adhesion inhibition;
KW thrombotic thrombocytopenic purpura; platelet aggregation inhibition;
KW idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;
KW thrombolytic; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004005890-A2.
XX
PD 15-JAN-2004.
XX
PF 03-JUL-2003; 2003WO-US021304.
XX
PR 03-JUL-2002; 2002US-0394352P.
PR 18-SEP-2002; 2002US-0411694P.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Siegel DL;
XX
DR WPI; 2004-142998/14.
DR N-PSDB; ADI22085.
XX
PS Claim 12; SEQ ID NO 101; 232pp; English.
XX
CC The present invention describes a method (M1) for identifying an anti-
CC platelet autoantibody (I) in a mammal. The autoantibody is detected by
CC producing an antibody phage display library from B-lymphocytes obtained
CC from the mammal, and screening the library to detect a phage that
CC specifically binds with a platelet component, where the screening
CC comprises panning the phage on intact platelets using competitive cell-
CC surface panning. Also described: (1) an autoantibody identified by (M1);
CC (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3)
CC inhibiting (M2) blood clotting in a mammal having a thrombus or at risk
CC of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a
CC mammal having a thrombus or at risk of thrombus formation; (5) inhibiting
CC (M4) binding of an anti-platelet autoantibody with a platelet component;
CC (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6)
CC thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7)
CC platelet aggregation; (9) inhibiting (M8) platelet activation; (10)
CC inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an
CC anti-platelet autoantibody, or its biologically active fragment with a
CC platelet; (12) identifying (M11) a peptide that inhibits binding of an
CC anti-platelet autoantibody with a platelet; (13) a peptide identified by
CC the method of (12); (14) a peptide that specifically binds with an anti-
CC platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic
CC purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood
CC clotting, inhibiting platelet aggregation, inhibiting platelet function
CC or inhibiting platelet activation comprising an amount of an anti-
CC platelet autoantibody, or its biologically active fragment that
CC specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or
CC its fragment comprises an antigen binding region derived from an H44L4
CC anti-platelet autoantibody, the kit further comprising a peptide
CC inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator
CC and an instructions for use. (I) has haemostatic, anticoagulant and
CC thrombolytic activities. The autoantibodies (I) are useful for diagnosing
CC and for developing therapeutics for diseases mediated by autoantibody
CC binding with platelet antigens. (M6) and (M12) are useful for treating
CC thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic
CC purpura, respectively. (M2) and (M3) are useful for inhibiting blood
CC clotting. The present sequence is used in the exemplification of the
CC present invention.
XX
SQ Sequence 108 AA;

```
  Query Match             95.8%;  Score 541;  DB 8;  Length 108;
  Best Local Similarity   95.4%;  Pred. No. 8.8e-36;
  Matches  103;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||| ||| ||:::||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPITFGQGTRLEIK 108
```

RESULT 20
ADF11403
ID ADF11403 standard; protein; 109 AA.
XX
AC ADF11403;
XX
DT 12-FEB-2004 (first entry)
XX
DE 2D8 anti-OPGL antibody kappa chain variable region SEQ ID NO:16.
XX
KW human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.
XX
OS Homo sapiens.
XX
PN WO2003086289-A2.
XX
PD 23-OCT-2003.
XX
PF 07-APR-2003; 2003WO-US010749.
XX
PR 05-APR-2002; 2002US-0370407P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;
XX
DR WPI; 2003-845253/78.
DR N-PSDB; ADF11402.
XX
PT New isolated antibody that specifically binds osteoprotegerin ligand,
PT useful for diagnosing or treating bone disorders, such as osteoporosis,
PT bone loss from arthritis, Paget's disease or osteopenia.
XX
PS Claim 6; SEQ ID NO 16; 156pp; English.
XX
CC The present invention describes an isolated human antibody (I) that
CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
CC pharmaceutical composition comprising a pharmaceutical carrier and a
CC therapeutic amount of (I); (2) methods of treating an osteopenic disorder
CC in a patient, comprising administering to a patient the pharmaceutical
CC composition of (1) or a pharmaceutical amount of (I); and (3) a method
CC for detecting OPGL in a biological sample, comprising contacting the
CC sample with (I) under conditions that allow for binding of the antibody
CC to OPGL, and measuring the level of bound antibody in the sample. (I) has
CC osteopathic, antiarthritic and cytostatic activities, and can be used in
CC gene therapy. The composition and methods are useful in diagnosing or
CC treating bone disorders, such as osteoporosis, bone loss from arthritis,
CC Paget's disease or osteopenia. The antibody (I) may also be used for
CC detecting OPGL in biological samples and in identifying cells or tissues
CC that produce the protein. The present sequence represents a sequence

```
CC   which is used in the exemplification of the present invention.
XX
SQ   Sequence 109 AA;

  Query Match            95.6%;  Score 540;  DB 7;  Length 109;
  Best Local Similarity  94.4%;  Pred. No. 1.1e-35;
  Matches  102;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSISSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||| |||:||| |||::||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSKWPPYTFGQGTKLEIK 108


RESULT 21
ADF11415
ID   ADF11415 standard; protein; 109 AA.
XX
AC   ADF11415;
XX
DT   12-FEB-2004  (first entry)
XX
DE   9H7 anti-OPGL antibody kappa chain variable region SEQ ID NO:28.
XX
KW   human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
KW   osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
KW   osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.
XX
OS   Homo sapiens.
XX
PN   WO2003086289-A2.
XX
PD   23-OCT-2003.
XX
PF   07-APR-2003; 2003WO-US010749.
XX
PR   05-APR-2002; 2002US-0370407P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boyle WJ,  Medlock E,  Sullivan JK,  Elliott RL,  Martin F,  Huang H;
XX
DR   WPI; 2003-845253/78.
DR   N-PSDB; ADF11414.
XX
PT   New isolated antibody that specifically binds osteoprotegerin ligand,
PT   useful for diagnosing or treating bone disorders, such as osteoporosis,
PT   bone loss from arthritis, Paget's disease or osteopenia.
XX
PS   Claim 6; SEQ ID NO 28; 156pp; English.
XX
CC   The present invention describes an isolated human antibody (I) that
CC   specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
CC   pharmaceutical composition comprising a pharmaceutical carrier and a
CC   therapeutic amount of (I); (2) methods of treating an osteopenic disorder
CC   in a patient, comprising administering to a patient the pharmaceutical
CC   composition of (1) or a pharmaceutical amount of (I); and (3) a method
CC   for detecting OPGL in a biological sample, comprising contacting the
CC   sample with (I) under conditions that allow for binding of the antibody
CC   to OPGL, and measuring the level of bound antibody in the sample. (I) has
CC   osteopathic, antiarthritic and cytostatic activities, and can be used in
CC   gene therapy. The composition and methods are useful in diagnosing or
CC   treating bone disorders, such as osteoporosis, bone loss from arthritis,
CC   Paget's disease or osteopenia. The antibody (I) may also be used for
CC   detecting OPGL in biological samples and in identifying cells or tissues
CC   that produce the protein. The present sequence represents a sequence
CC   which is used in the exemplification of the present invention.
XX
SQ   Sequence 109 AA;

  Query Match            95.6%;  Score 540;  DB 7;  Length 109;
  Best Local Similarity  94.4%;  Pred. No. 1.1e-35;
  Matches  102;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSISSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||| |||:||| |||::||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSKWPPYTFGQGTKLEIK 108


RESULT 22
ADF11439
ID   ADF11439 standard; protein; 215 AA.
XX
AC   ADF11439;
XX
DT   12-FEB-2004  (first entry)
XX
DE   9H7 anti-OPGL antibody light chain SEQ ID NO:52.
XX
KW   human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
KW   osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
KW   osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.
XX
OS   Homo sapiens.
XX
PN   WO2003086289-A2.
XX
PD   23-OCT-2003.
XX
PF   07-APR-2003; 2003WO-US010749.
XX
PR   05-APR-2002; 2002US-0370407P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boyle WJ,  Medlock E,  Sullivan JK,  Elliott RL,  Martin F,  Huang H;
XX
DR   WPI; 2003-845253/78.
DR   N-PSDB; ADF11438.
XX
PT   New isolated antibody that specifically binds osteoprotegerin ligand,
PT   useful for diagnosing or treating bone disorders, such as osteoporosis,
PT   bone loss from arthritis, Paget's disease or osteopenia.
XX
PS   Claim 16; SEQ ID NO 52; 156pp; English.
XX
CC   The present invention describes an isolated human antibody (I) that
CC   specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
CC   pharmaceutical composition comprising a pharmaceutical carrier and a
CC   therapeutic amount of (I); (2) methods of treating an osteopenic disorder
CC   in a patient, comprising administering to a patient the pharmaceutical
CC   composition of (1) or a pharmaceutical amount of (I); and (3) a method
CC   for detecting OPGL in a biological sample, comprising contacting the
CC   sample with (I) under conditions that allow for binding of the antibody
CC   to OPGL, and measuring the level of bound antibody in the sample. (I) has
CC   osteopathic, antiarthritic and cytostatic activities, and can be used in
CC   gene therapy. The composition and methods are useful in diagnosing or
CC   treating bone disorders, such as osteoporosis, bone loss from arthritis,
CC   Paget's disease or osteopenia. The antibody (I) may also be used for
CC   detecting OPGL in biological samples and in identifying cells or tissues
CC   that produce the protein. The present sequence represents a sequence
CC   which is used in the exemplification of the present invention.
XX
SQ   Sequence 215 AA;

  Query Match            95.6%;  Score 540;  DB 7;  Length 215;
  Best Local Similarity  94.4%;  Pred. No. 2e-35;
  Matches  102;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSISSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||| |||:||| |||::||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSKWPPYTFGQGTKLEIK 108
```

RESULT 23
ADF11427
ID ADF11427 standard; protein; 215 AA.
XX
AC ADF11427;
XX
DT 12-FEB-2004 (first entry)
XX
DE 2D8 anti-OPGL antibody light chain SEQ ID NO:40.
XX
KW human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.
XX
OS Homo sapiens.
XX
PN WO2003086289-A2.
XX
PD 23-OCT-2003.
XX
PF 07-APR-2003; 2003WO-US010749.
XX
PR 05-APR-2002; 2002US-0370407P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;
XX
DR WPI; 2003-845253/78.
DR N-PSDB; ADF11426.
XX
PT New isolated antibody that specifically binds osteoprotegerin ligand,
PT useful for diagnosing or treating bone disorders, such as osteoporosis,
PT bone loss from arthritis, Paget's disease or osteopenia.
XX
PS Claim 16; SEQ ID NO 40; 156pp; English.
XX
CC The present invention describes an isolated human antibody (I) that
CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
CC pharmaceutical composition comprising a pharmaceutical carrier and a
CC therapeutic amount of (I); (2) methods of treating an osteopenic disorder
CC in a patient, comprising administering to a patient the pharmaceutical
CC composition of (1) or a pharmaceutical amount of (I); and (3) a method
CC for detecting OPGL in a biological sample, comprising contacting the
CC sample with (I) under conditions that allow for binding of the antibody
CC to OPGL, and measuring the level of bound antibody in the sample. (I) has
CC osteopathic, antiarthritic and cytostatic activities, and can be used in
CC gene therapy. The composition and methods are useful in diagnosing or
CC treating bone disorders, such as osteoporosis, bone loss from arthritis,
CC Paget's disease or osteopenia. The antibody (I) may also be used for
CC detecting OPGL in biological samples and in identifying cells or tissues
CC that produce the protein. The present sequence represents a sequence
CC which is used in the exemplification of the present invention.
XX
SQ Sequence 215 AA;

Query Match 95.6%; Score 540; DB 7; Length 215;
Best Local Similarity 94.4%; Pred. No. 2e-35;
Matches 102; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSISSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||| |||:||| |||::||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSKWPPYTFGQGTKLEIK 108
```

RESULT 24
ABP57362
ID ABP57362 standard; protein; 129 AA.
XX
AC ABP57362;
XX
DT 22-APR-2003 (first entry)
XX
DE Anti-TRAIL-R antibody related clone E-11-13 protein SEQ ID NO:19.
XX
KW Human; TRAIL-R1; TRAIL-R2; antibody; cytostatic; apoptotic; tumour;
KW antibody therapy.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200294880-A1.
XX
PD 28-NOV-2002.
XX
PF 17-MAY-2002; 2002WO-JP004816.
XX
PR 18-MAY-2001; 2001JP-00150213.
PR 09-AUG-2001; 2001JP-00243040.
PR 11-OCT-2001; 2001JP-00314489.
XX
PA (KIRI) KIRIN BEER KK.
XX
PI Mori E, Kataoka S;
XX
DR WPI; 2003-120790/11.
DR N-PSDB; ABZ59693.
XX
PT New anti-TRAIL-R antibodies with activity of inducing apoptosis of cancer
PT cells and without exerting an effect on normal cells expressing TRAIL-Rs
PT nor inducing injury to hepatocytes, for use in therapy of malignant
PT tumor.
XX
PS Claim 54; Page 56; 92pp; Japanese.
XX
CC The present invention describes antibodies or their functional fragments
CC that bind to TRAIL-R1 and/or TRAIL-R2. TRAIL-R1 and TRAIL-R2 antibodies
CC have cytostatic and apoptotic activities, and can be used in antibody
CC therapy. The antibodies can be applied as remedies and preventives of
CC diseases due to cells expressing TRAIL-R1 and TRAIL-R2, which are useful
CC in the therapy of malignant tumours. Remedies produced with the
CC antibodies are highly safe, and avoid hepatotoxicity. The present
CC sequence represents an anti-TRAIL-R antibody amino acid sequence from the
CC present invention
XX
SQ Sequence 129 AA;

Query Match 95.1%; Score 537.5; DB 6; Length 129;
Best Local Similarity 97.2%; Pred. No. 2e-35;
Matches 105; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

```
Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db         21 EIVLTQSPATLSLSPGERATLSCRASQSVSSFLAWYQQKPGQAPRLLIYDASNRATGIPA 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||| | ||||||||||
Db         81 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNW-PLTFGPGTKVDIK 127
```

RESULT 25
ABR54916
ID ABR54916 standard; protein; 107 AA.

XX
AC ABR54916;
XX
DT 30-JUN-2003 (first entry)
XX
DE Light chain clone HBPAXK9b 3E7 SEQ ID NO:142.
XX
KW Engineered template; single primer amplification; antibody library;
KW nucleic acid amplification.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003025202-A2.
XX
PD 27-MAR-2003.
XX
PF 19-SEP-2002; 2002WO-US029889.
XX
PR 19-SEP-2001; 2001US-0323455P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Frederickson S, Maruyama T, Lin Y, Renshaw M;
XX
DR WPI; 2003-313359/30.
XX
PT Amplifying nucleic acid by contacting engineered nucleic acid strand
PT having predetermined sequence at one end and sequence complementary to
PT predetermined sequence at other end, with primer having predetermined
PT sequence.
XX
PS Example 3; Fig 8b-c; 68pp; English.
XX
CC The present invention describes a method (M1) for amplifying a nucleic
CC acid strand. M1 comprises providing an engineered nucleic acid strand (S)
CC having a predetermined sequence at one end and a sequence complementary
CC to the predetermined sequence at the other, and contacting (S) with a
CC primer having the predetermined sequence in the presence of a polymers
CC and nucleotides under conditions suitable for polymerisation of the
CC nucleotides. Also described is an engineered nucleic acid strand (I)
CC having a predetermined sequence at one end and a sequence complementary
CC to the predetermined sequence at the other end. M1 is useful for
CC amplifying a nucleic acid. M1 can be used for producing an antibody
CC library. M1 is useful for preparing amplified products that can be
CC ligated into a suitable expression vector, where the vector can be used
CC to transform an appropriate host organism to produce the polypeptide or
CC protein encoded by the target sequence. M1 is useful to amplify a family
CC of related sequences to build a complex library such as, for example an
CC antibody library. M1 is useful not only for producing large amounts of
CC one target nucleic acid sequence, but also for amplifying simultaneously
CC more than one different target nucleic acid sequence located on the same
CC or different nucleic acid molecules. ACC62635 to ACC62753 and ABR54841 to
CC ABR54998 represent sequence used in the exemplification of the present
CC invention
XX
SQ Sequence 107 AA;

Query Match 94.8%; Score 535.5; DB 6; Length 107;
Best Local Similarity 97.2%; Pred. No. 2.4e-35;
Matches 105; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

```
Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||||| ||| ||||:||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPP-TFGGGTKVEIK 107
```

Search completed: June 16, 2005, 07:43:02
Job time : 116.812 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 07:43:15 ; Search time 100.735 Seconds
(without alignments)
411.670 Million cell updates/sec

Title: US-09-920-137D-8
Perfect score: 565
Sequence: 1 EIVLTQSPATLSLSPGERAT.....QQRSNWPPFTFGPGTKVDIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	565	100.0	108	10	US-09-920-267C-8	Sequence 8, Appli
2	565	100.0	108	14	US-10-305-347A-8	Sequence 8, Appli
3	565	100.0	108	16	US-10-720-323-8	Sequence 8, Appli
4	565	100.0	108	18	US-10-954-900A-8	Sequence 8, Appli
5	547	96.8	109	15	US-10-408-901-24	Sequence 24, Appl
6	547	96.8	215	15	US-10-408-901-48	Sequence 48, Appl
7	546	96.6	128	15	US-10-656-769-12	Sequence 12, Appl
8	546	96.6	130	16	US-10-394-471B-16	Sequence 16, Appl
9	546	96.6	235	15	US-10-656-769-38	Sequence 38, Appl
10	544	96.3	108	15	US-10-173-551-9	Sequence 9, Appli
11	542	95.9	108	17	US-10-886-838-4	Sequence 4, Appli
12	542	95.9	109	15	US-10-408-901-8	Sequence 8, Appli
13	542	95.9	215	15	US-10-408-901-32	Sequence 32, Appl
14	540	95.6	109	15	US-10-408-901-16	Sequence 16, Appl
15	540	95.6	109	15	US-10-408-901-28	Sequence 28, Appl
16	540	95.6	215	15	US-10-408-901-40	Sequence 40, Appl
17	540	95.6	215	15	US-10-408-901-52	Sequence 52, Appl
18	537.5	95.1	129	16	US-10-478-056-19	Sequence 19, Appl
19	535.5	94.8	107	15	US-10-251-085B-142	Sequence 142, App
20	535.5	94.8	107	16	US-10-737-252-142	Sequence 142, App
21	535.5	94.8	236	17	US-10-961-567A-6	Sequence 6, Appli
22	535	94.7	251	10	US-09-880-748-1049	Sequence 1049, Ap
23	535	94.7	251	15	US-10-293-418-1049	Sequence 1049, Ap
24	530.5	93.9	107	17	US-10-891-658-91	Sequence 91, Appl
25	530	93.8	108	17	US-10-886-838-2	Sequence 2, Appli
26	529.5	93.7	107	10	US-09-791-153A-69	Sequence 69, Appl
27	529.5	93.7	224	10	US-09-453-234-46	Sequence 46, Appl
28	529	93.6	130	15	US-10-443-466A-25	Sequence 25, Appl
29	528.5	93.5	107	10	US-09-791-153A-71	Sequence 71, Appl
30	528.5	93.5	107	10	US-09-982-464-2	Sequence 2, Appli
31	528.5	93.5	107	16	US-10-697-399-2	Sequence 2, Appli
32	528.5	93.5	107	17	US-10-697-400-2	Sequence 2, Appli
33	528.5	93.5	107	17	US-10-911-838-14	Sequence 14, Appl
34	528.5	93.5	107	17	US-10-911-838-21	Sequence 21, Appl
35	528.5	93.5	128	16	US-10-478-056-31	Sequence 31, Appl
36	528.5	93.5	139	16	US-10-687-799-55	Sequence 55, Appl
37	526.5	93.2	129	16	US-10-478-056-23	Sequence 23, Appl
38	524.5	92.8	224	10	US-09-453-234-82	Sequence 82, Appl
39	524.5	92.8	224	10	US-09-453-234-88	Sequence 88, Appl
40	524.5	92.8	224	10	US-09-453-234-90	Sequence 90, Appl
41	524	92.7	108	15	US-10-173-551-19	Sequence 19, Appl
42	523.5	92.7	107	15	US-10-251-085B-143	Sequence 143, App
43	523.5	92.7	107	16	US-10-737-252-143	Sequence 143, App
44	523.5	92.7	127	16	US-10-687-799-4	Sequence 4, Appli
45	523.5	92.7	127	16	US-10-687-799-8	Sequence 8, Appli
46	523.5	92.7	127	16	US-10-687-799-12	Sequence 12, Appl
47	523.5	92.7	127	16	US-10-687-799-57	Sequence 57, Appl
48	523.5	92.7	224	10	US-09-453-234-36	Sequence 36, Appl
49	522	92.4	126	16	US-10-693-629-30	Sequence 30, Appl
50	521.5	92.3	107	17	US-10-982-359-65	Sequence 65, Appl
51	520.5	92.1	224	10	US-09-453-234-84	Sequence 84, Appl
52	517.5	91.6	107	14	US-10-181-324-4	Sequence 4, Appli
53	516.5	91.4	107	15	US-10-251-085B-141	Sequence 141, App
54	516.5	91.4	107	16	US-10-737-252-141	Sequence 141, App
55	516.5	91.4	107	17	US-10-937-596-27	Sequence 27, Appl
56	516	91.3	129	16	US-10-693-629-34	Sequence 34, Appl
57	515.5	91.2	107	14	US-10-233-996-40	Sequence 40, Appl
58	515.5	91.2	107	15	US-10-338-366-8	Sequence 8, Appli
59	514.5	91.1	109	17	US-10-484-790A-2	Sequence 2, Appli
60	514.5	91.1	214	17	US-10-484-790A-19	Sequence 19, Appl
61	512.5	90.7	113	15	US-10-374-600-21	Sequence 21, Appl
62	512.5	90.7	113	15	US-10-374-531-21	Sequence 21, Appl
63	512	90.6	109	15	US-10-371-942-72	Sequence 72, Appl
64	512	90.6	109	15	US-10-371-942-76	Sequence 76, Appl
65	509.5	90.2	107	17	US-10-891-658-89	Sequence 89, Appl
66	508.5	90.0	236	11	US-09-833-245-237	Sequence 237, App
67	504.5	89.3	234	15	US-10-045-674-587	Sequence 587, App
68	503	89.0	125	16	US-10-693-629-54	Sequence 54, Appl
69	499.5	88.4	226	10	US-09-453-234-38	Sequence 38, Appl
70	498.5	88.2	107	14	US-10-269-805-62	Sequence 62, Appl
71	497.5	88.1	110	17	US-10-726-332-213	Sequence 213, App
72	497.5	88.1	234	10	US-09-848-832-4	Sequence 4, Appli
73	497.5	88.1	234	14	US-10-225-108A-4	Sequence 4, Appli
74	497.5	88.1	234	15	US-10-461-148-2	Sequence 2, Appli
75	496.5	87.9	107	14	US-10-091-300-26	Sequence 26, Appl
76	496.5	87.9	107	16	US-10-482-630-78	Sequence 78, Appl
77	495.5	87.7	107	17	US-10-727-155-314	Sequence 314, App
78	495.5	87.7	107	17	US-10-938-353-107	Sequence 107, App
79	495	87.6	117	14	US-10-300-675-4	Sequence 4, Appli
80	495	87.6	117	17	US-10-910-124-4	Sequence 4, Appli
81	493	87.3	95	14	US-10-194-975-86	Sequence 86, Appl
82	493	87.3	95	15	US-10-308-817-33	Sequence 33, Appl
83	493	87.3	95	15	US-10-453-698-33	Sequence 33, Appl
84	493	87.3	95	16	US-10-379-392-93	Sequence 93, Appl

85	493	87.3	117	14	US-10-300-675-38	Sequence 38, Appl
86	492	87.1	105	8	US-08-844-215-9	Sequence 9, Appli
87	491.5	87.0	108	15	US-10-371-942-68	Sequence 68, Appl
88	491.5	87.0	226	10	US-09-453-234-72	Sequence 72, Appl
89	490.5	86.8	129	15	US-10-309-764-141	Sequence 141, App
90	489.5	86.6	107	15	US-10-251-085B-117	Sequence 117, App
91	489.5	86.6	107	15	US-10-251-085B-119	Sequence 119, App
92	489.5	86.6	107	16	US-10-737-252-117	Sequence 117, App
93	489.5	86.6	107	16	US-10-737-252-119	Sequence 119, App
94	489	86.5	110	14	US-10-001-934-40	Sequence 40, Appl
95	489	86.5	110	15	US-10-275-046-69	Sequence 69, Appl
96	488	86.4	108	15	US-10-251-085B-132	Sequence 132, App
97	488	86.4	108	16	US-10-737-252-132	Sequence 132, App
98	488	86.4	117	14	US-10-300-675-28	Sequence 28, Appl
99	488	86.4	117	14	US-10-300-675-30	Sequence 30, Appl
100	488	86.4	117	14	US-10-300-675-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-09-920-267C-8
; Sequence 8, Application US/09920267C
; Publication No. US20030040044A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249
; CURRENT APPLICATION NUMBER: US/09/920,267C
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-267C-8

Query Match 100.0%; Score 565; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.2e-41;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
```

RESULT 2
US-10-305-347A-8
; Sequence 8, Application US/10305347A
; Publication No. US20030143603A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Bernie Scallon
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5005
; CURRENT APPLICATION NUMBER: US/10/305,347A
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-305-347A-8

Query Match 100.0%; Score 565; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.2e-41;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
```

RESULT 3
US-10-720-323-8
; Sequence 8, Application US/10720323
; Publication No. US20040185507A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249 CIPNP
; CURRENT APPLICATION NUMBER: US/10/720,323
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-720-323-8

Query Match 100.0%; Score 565; DB 16; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.2e-41;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
```

RESULT 4
US-10-954-900A-8
; Sequence 8, Application US/10954900A
; Publication No. US20050123541A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: David Shealy
; APPLICANT: David Knight
; APPLICANT: Bernie Scallon
; APPLICANT: George Heavner
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0250 DIV-2
; CURRENT APPLICATION NUMBER: US/10/954,900A
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 09/920,262
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,360
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,826

```
;  PRIOR FILING DATE: 2000-09-29
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 8
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-954-900A-8

  Query Match             100.0%;  Score 565;  DB 18;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-41;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108


RESULT 5
US-10-408-901-24
; Sequence 24, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
;  APPLICANT: Boyle, William
;  APPLICANT:  Huang, Haichun
;  APPLICANT:  Elliot, Robin
;  APPLICANT:  Sullivan, John
;  APPLICANT:  Medlock, Eugene
;  APPLICANT:  Martin, Francis
;  TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: MBHB 01-1145-A
;  CURRENT APPLICATION NUMBER: US/10/408,901
;  CURRENT FILING DATE:  2003-04-07
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-901-24

  Query Match             96.8%;  Score 547;  DB 15;  Length 109;
  Best Local Similarity   96.3%;  Pred. No. 8e-40;
  Matches  104;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||:||| |||::||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPYTFGQGTKLEIK 108


RESULT 6
US-10-408-901-48
; Sequence 48, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
;  APPLICANT: Boyle, William
;  APPLICANT:  Huang, Haichun
;  APPLICANT:  Elliot, Robin
;  APPLICANT:  Sullivan, John
;  APPLICANT:  Medlock, Eugene
;  APPLICANT:  Martin, Francis
;  TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: MBHB 01-1145-A
;  CURRENT APPLICATION NUMBER: US/10/408,901
;  CURRENT FILING DATE:  2003-04-07
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-901-48

  Query Match             96.8%;  Score 547;  DB 15;  Length 215;
  Best Local Similarity   96.3%;  Pred. No. 1.5e-39;
  Matches  104;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||:||| |||::||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPYTFGQGTKLEIK 108


RESULT 7
US-10-656-769-12
; Sequence 12, Application US/10656769
; Publication No. US20040097712A1
; GENERAL INFORMATION:
;  APPLICANT: Varnum, Brian
;  APPLICANT:  Witte, Alison
;  APPLICANT:  Vezina, Chris
;  APPLICANT:  Wong, Lu Min
;  APPLICANT:  Qian, Xueming
;  TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
;  FILE REFERENCE: 01,1554
;  CURRENT APPLICATION NUMBER: US/10/656,769
;  CURRENT FILING DATE:  2003-09-05
;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
;   LENGTH: 128
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-656-769-12

  Query Match             96.6%;  Score 546;  DB 15;  Length 128;
  Best Local Similarity   97.2%;  Pred. No. 1.1e-39;
  Matches  105;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||| ||| ||||:||
Db         81 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPLTFGGGTKVEIK 128


RESULT 8
US-10-394-471B-16
; Sequence 16, Application US/10394471B
; Publication No. US20040185047A1
; GENERAL INFORMATION:
;  APPLICANT: Giles-Komar, Jill; Carton, Jill; Scallon, Bernard J.
;  TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
;  FILE REFERENCE: CEN0202
;  CURRENT APPLICATION NUMBER: US/10/394,471B
;  CURRENT FILING DATE:  2003-03-21
;  PRIOR APPLICATION NUMBER: 60/367,903
;  PRIOR FILING DATE: 2002-03-26
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 16
```

```
;   LENGTH: 130
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-394-471B-16

  Query Match             96.6%;  Score 546;  DB 16;  Length 130;
  Best Local Similarity   97.2%;  Pred. No. 1.2e-39;
  Matches  105;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||| ||| ||||:||
Db         81 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPLTFGGGTKVEIK 128


RESULT 9
US-10-656-769-38
; Sequence 38, Application US/10656769
; Publication No. US20040097712A1
; GENERAL INFORMATION:
;  APPLICANT: Varnum, Brian
;  APPLICANT:  Witte, Alison
;  APPLICANT:  Vezina, Chris
;  APPLICANT:  Wong, Lu Min
;  APPLICANT:  Qian, Xueming
;  TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
;  FILE REFERENCE: 01,1554
;  CURRENT APPLICATION NUMBER: US/10/656,769
;  CURRENT FILING DATE:  2003-09-05
;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
;   LENGTH: 235
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-656-769-38

  Query Match             96.6%;  Score 546;  DB 15;  Length 235;
  Best Local Similarity   97.2%;  Pred. No. 2.1e-39;
  Matches  105;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||| ||| ||||:||
Db         81 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPLTFGGGTKVEIK 128


RESULT 10
US-10-173-551-9
; Sequence 9, Application US/10173551
; Publication No. US20030232387A1
; GENERAL INFORMATION:
;  APPLICANT: Lu, Chafen
;  TITLE OF INVENTION: Antibodies that bind alphaE Integrin
;  FILE REFERENCE: 1855.2025-000
;  CURRENT APPLICATION NUMBER: US/10/173,551
;  CURRENT FILING DATE:  2002-06-14
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (24)...(34)
;   OTHER INFORMATION: CDR1
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (50)...(56)
;   OTHER INFORMATION: CDR2
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (89)...(98)
;   OTHER INFORMATION: CDR3
US-10-173-551-9

  Query Match             96.3%;  Score 544;  DB 15;  Length 108;
  Best Local Similarity   97.2%;  Pred. No. 1.4e-39;
  Matches  105;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||| ||| ||||:||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPGTFGQGTKVEIK 108


RESULT 11
US-10-886-838-4
; Sequence 4, Application US/10886838
; Publication No. US20050008642A1
; GENERAL INFORMATION:
;  APPLICANT: Hoffmann-La Roche Inc.
;  TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and uses
;  TITLE OF INVENTION:  thereof
;  FILE REFERENCE: 21695
;  CURRENT APPLICATION NUMBER: US/10/886,838
;  CURRENT FILING DATE:  2004-07-08
;  PRIOR APPLICATION NUMBER: EP 03015526
;  PRIOR FILING DATE: 2003-07-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-886-838-4

  Query Match             95.9%;  Score 542;  DB 17;  Length 108;
  Best Local Similarity   96.3%;  Pred. No. 2.1e-39;
  Matches  104;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||| |||:||| ||||:||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSKWPPWTFGQGTKVEIK 108


RESULT 12
US-10-408-901-8
; Sequence 8, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
;  APPLICANT: Boyle, William
;  APPLICANT:  Huang, Haichun
;  APPLICANT:  Elliot, Robin
;  APPLICANT:  Sullivan, John
;  APPLICANT:  Medlock, Eugene
;  APPLICANT:  Martin, Francis
;  TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: MBHB 01-1145-A
;  CURRENT APPLICATION NUMBER: US/10/408,901
;  CURRENT FILING DATE:  2003-04-07
```

```
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-901-8

  Query Match             95.9%;  Score 542;  DB 15;  Length 109;
  Best Local Similarity   94.4%;  Pred. No. 2.2e-39;
  Matches  102;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||:|||||:||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVNSYLAWFQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||:||||||||||||| |||::||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAIYYCQQRSNWPPFTFGQGTKLEIK 108


RESULT 13
US-10-408-901-32
; Sequence 32, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
;  APPLICANT: Boyle, William
;  APPLICANT:  Huang, Haichun
;  APPLICANT:  Elliot, Robin
;  APPLICANT:  Sullivan, John
;  APPLICANT:  Medlock, Eugene
;  APPLICANT:  Martin, Francis
;  TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: MBHB 01-1145-A
;  CURRENT APPLICATION NUMBER: US/10/408,901
;  CURRENT FILING DATE:  2003-04-07
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-901-32

  Query Match             95.9%;  Score 542;  DB 15;  Length 215;
  Best Local Similarity   94.4%;  Pred. No. 4.2e-39;
  Matches  102;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||:|||||:||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVNSYLAWFQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||:||||||||||||| |||::||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAIYYCQQRSNWPPFTFGQGTKLEIK 108


RESULT 14
US-10-408-901-16
; Sequence 16, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
;  APPLICANT: Boyle, William
;  APPLICANT:  Huang, Haichun
;  APPLICANT:  Elliot, Robin
;  APPLICANT:  Sullivan, John
;  APPLICANT:  Medlock, Eugene
;  APPLICANT:  Martin, Francis
;  TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: MBHB 01-1145-A
;  CURRENT APPLICATION NUMBER: US/10/408,901
;  CURRENT FILING DATE:  2003-04-07
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-901-16

  Query Match             95.6%;  Score 540;  DB 15;  Length 109;
  Best Local Similarity   94.4%;  Pred. No. 3.2e-39;
  Matches  102;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSISSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||| |||:||| |||::||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSKWPPYTFGQGTKLEIK 108


RESULT 15
US-10-408-901-28
; Sequence 28, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
;  APPLICANT: Boyle, William
;  APPLICANT:  Huang, Haichun
;  APPLICANT:  Elliot, Robin
;  APPLICANT:  Sullivan, John
;  APPLICANT:  Medlock, Eugene
;  APPLICANT:  Martin, Francis
;  TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: MBHB 01-1145-A
;  CURRENT APPLICATION NUMBER: US/10/408,901
;  CURRENT FILING DATE:  2003-04-07
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-901-28

  Query Match             95.6%;  Score 540;  DB 15;  Length 109;
  Best Local Similarity   94.4%;  Pred. No. 3.2e-39;
  Matches  102;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSISSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||| |||:||| |||::||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSKWPPYTFGQGTKLEIK 108


RESULT 16
US-10-408-901-40
; Sequence 40, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
;  APPLICANT: Boyle, William
;  APPLICANT:  Huang, Haichun
;  APPLICANT:  Elliot, Robin
;  APPLICANT:  Sullivan, John
;  APPLICANT:  Medlock, Eugene
;  APPLICANT:  Martin, Francis
;  TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: MBHB 01-1145-A
```

```
;  CURRENT APPLICATION NUMBER: US/10/408,901
;  CURRENT FILING DATE:  2003-04-07
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-901-40

  Query Match             95.6%;  Score 540;  DB 15;  Length 215;
  Best Local Similarity   94.4%;  Pred. No. 6.2e-39;
  Matches  102;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSISSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||| |||:||| |||::||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSKWPPYTFGQGTKLEIK 108


RESULT 17
US-10-408-901-52
; Sequence 52, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
;  APPLICANT: Boyle, William
;  APPLICANT:  Huang, Haichun
;  APPLICANT:  Elliot, Robin
;  APPLICANT:  Sullivan, John
;  APPLICANT:  Medlock, Eugene
;  APPLICANT:  Martin, Francis
;  TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
;  TITLE OF INVENTION:  Inhibitors
;  FILE REFERENCE: MBHB 01-1145-A
;  CURRENT APPLICATION NUMBER: US/10/408,901
;  CURRENT FILING DATE:  2003-04-07
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 52
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-901-52

  Query Match             95.6%;  Score 540;  DB 15;  Length 215;
  Best Local Similarity   94.4%;  Pred. No. 6.2e-39;
  Matches  102;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSISSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||| |||:||| |||::||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSKWPPYTFGQGTKLEIK 108


RESULT 18
US-10-478-056-19
; Sequence 19, Application US/10478056
; Publication No. US20040214235A1
; GENERAL INFORMATION:
;  APPLICANT: KIRIN BEER KABUSHIKI KAISHA
;  TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
;  FILE REFERENCE: PH-1573-PCT
;  CURRENT APPLICATION NUMBER: US/10/478,056
;  CURRENT FILING DATE:  2003-11-18
;  PRIOR APPLICATION NUMBER: JP2001-150213
;  PRIOR FILING DATE: 2001-05-18
;  PRIOR APPLICATION NUMBER: JP2001-243040
;  PRIOR FILING DATE: 2001-08-09
;  PRIOR APPLICATION NUMBER: JP2001-314489
;  PRIOR FILING DATE: 2001-10-11
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-478-056-19

  Query Match             95.1%;  Score 537.5;  DB 16;  Length 129;
  Best Local Similarity   97.2%;  Pred. No. 6.2e-39;
  Matches  105;  Conservative    1;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db         21 EIVLTQSPATLSLSPGERATLSCRASQSVSSFLAWYQQKPGQAPRLLIYDASNRATGIPA 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||| | ||||||||||
Db         81 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNW-PLTFGPGTKVDIK 127


RESULT 19
US-10-251-085B-142
; Sequence 142, Application US/10251085B
; Publication No. US20040072164A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Frederickson, Shana
;  APPLICANT:  Renshaw, Mark
;  APPLICANT:  Lin, Ying-Chi
;  APPLICANT:  Maruyama, Toshiaki
;  TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
;  FILE REFERENCE: 1087-21
;  CURRENT APPLICATION NUMBER: US/10/251,085B
;  CURRENT FILING DATE:  2002-09-19
;  PRIOR APPLICATION NUMBER: US 60/323,455
;  PRIOR FILING DATE: 2001-09-19
;  NUMBER OF SEQ ID NOS: 278
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 142
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: human
US-10-251-085B-142

  Query Match             94.8%;  Score 535.5;  DB 15;  Length 107;
  Best Local Similarity   97.2%;  Pred. No. 7.7e-39;
  Matches  105;  Conservative    1;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||| ||| ||||:||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPP-TFGGGTKVEIK 107


RESULT 20
US-10-737-252-142
; Sequence 142, Application US/10737252
; Publication No. US20040175736A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Frederickson, Shana
;  APPLICANT:  Renshaw, Mark
;  APPLICANT:  Lin, Ying-Chi
;  APPLICANT:  Maruyama, Toshiaki
;  TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
;  FILE REFERENCE: 1087-21 CIP
```

```
;  CURRENT APPLICATION NUMBER: US/10/737,252
;  CURRENT FILING DATE:  2003-12-15
;  PRIOR APPLICATION NUMBER: US 10/251,085
;  PRIOR FILING DATE: 2002-09-19
;  PRIOR APPLICATION NUMBER: US 60/323,455
;  PRIOR FILING DATE: 2001-09-19
;  NUMBER OF SEQ ID NOS: 309
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 142
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: human
US-10-737-252-142

  Query Match             94.8%;  Score 535.5;  DB 16;  Length 107;
  Best Local Similarity   97.2%;  Pred. No. 7.7e-39;
  Matches  105;  Conservative    1;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||| ||| ||||:||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPP-TFGGGTKVEIK 107


RESULT 21
US-10-961-567A-6
; Sequence 6, Application US/10961567A
; Publication No. US20050095244A1
; GENERAL INFORMATION:
;  APPLICANT: Jure-Kunkel, Maria
;  APPLICANT:  Hefta, Laura
;  APPLICANT:  Santoro, Marc
;  APPLICANT:  Ganguly, Subinay
;  TITLE OF INVENTION: FULLY HUMAN ANTIBODIES AGAINST HUMAN 4-1BB
;  FILE REFERENCE: 10060 NP
;  CURRENT APPLICATION NUMBER: US/10/961,567A
;  CURRENT FILING DATE:  2004-10-08
;  PRIOR APPLICATION NUMBER: US 60/510193
;  PRIOR FILING DATE: 2003-10-10
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
;   LENGTH: 236
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: pD16gate-20H4.9.LC amino acid sequence
US-10-961-567A-6

  Query Match             94.8%;  Score 535.5;  DB 17;  Length 236;
  Best Local Similarity   96.3%;  Pred. No. 1.7e-38;
  Matches  105;  Conservative    1;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPP-FTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||  ||| ||||:||
Db         81 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPALTFGGGTKVEIK 129


RESULT 22
US-09-880-748-1049
; Sequence 1049, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1049
;   LENGTH: 251
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-1049

  Query Match             94.7%;  Score 535;  DB 10;  Length 251;
  Best Local Similarity   96.3%;  Pred. No. 2e-38;
  Matches  104;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 202

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||  ||| ||||:||
Db        203 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPFLTFGGGTKVEIK 250


RESULT 23
US-10-293-418-1049
; Sequence 1049, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P2
;  CURRENT APPLICATION NUMBER: US/10/293,418
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-16
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1049
;   LENGTH: 251
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-293-418-1049

  Query Match             94.7%;  Score 535;  DB 15;  Length 251;
  Best Local Similarity   96.3%;  Pred. No. 2e-38;
  Matches  104;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 202
```

```
Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||||||||||||||||||||  ||| ||||:||
Db        203 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPFLTFGGGTKVEIK 250
```

RESULT 24
US-10-891-658-91
; Sequence 91, Application US/10891658
; Publication No. US20050074821A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth, Wild
; APPLICANT: Treanor, James
; APPLICANT: Huang, Haichun
; APPLICANT: Inoue, Heather
; APPLICANT: Zhang, Tie J.
; APPLICANT: Martin, Frank
; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: 02-1240
; CURRENT APPLICATION NUMBER: US/10/891,658
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/487,431
; PRIOR FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 91
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapien
US-10-891-658-91

Query Match 93.9%; Score 530.5; DB 17; Length 107;
Best Local Similarity 96.3%; Pred. No. 2.1e-38;
Matches 104; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

```
Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||||| |:||| ||||:||
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNW-PWTFGQGTKVEIK 107
```

RESULT 25
US-10-886-838-2
; Sequence 2, Application US/10886838
; Publication No. US20050008642A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and uses
; TITLE OF INVENTION: thereof
; FILE REFERENCE: 21695
; CURRENT APPLICATION NUMBER: US/10/886,838
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: EP 03015526
; PRIOR FILING DATE: 2003-07-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-886-838-2

Query Match 93.8%; Score 530; DB 17; Length 108;
Best Local Similarity 94.4%; Pred. No. 2.3e-38;
Matches 102; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASKRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||||| |||:||| ||||: |
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSKWPPWTFGQGTKVESK 108
```

Search completed: June 16, 2005, 08:01:34
Job time : 101.735 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 07:35:01 ; Search time 22.7623 Seconds
(without alignments)
456.518 Million cell updates/sec

Title: US-09-920-137D-8
Perfect score: 565
Sequence: 1 EIVLTQSPATLSLSPGERAT.....QQRSNWPPFTFGPGTKVDIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	534	94.5	114	2	S54905	Ig kappa chain V r
2	530.5	93.9	111	2	S23628	Ig kappa chain V r
3	525.5	93.0	144	2	PL0106	Ig kappa chain pre
4	523.5	92.7	128	2	A56701	Ig kappa chain V r
5	518.5	91.8	108	2	G44151	Ig kappa chain V r
6	514.5	91.1	128	2	S40345	Ig kappa chain V-J
7	513.5	90.9	129	2	S29627	Ig kappa chain V r
8	503.5	89.1	128	2	S40379	Ig kappa chain V-J
9	500.5	88.6	107	2	S57444	Ig kappa chain V-J
10	494.5	87.5	125	2	S40344	Ig kappa chain V-J
11	493	87.3	115	1	K3HUVG	Ig kappa chain pre
12	479.5	84.9	106	2	PC4282	Ig kappa chain (an
13	478.5	84.7	114	2	S46375	Ig kappa chain V-J
14	478	84.6	215	2	JE0244	Ig kappa chain NIG
15	477	84.4	115	2	S11697	Ig kappa chain pre
16	476.5	84.3	117	2	S40362	Ig kappa chain - h
17	473.5	83.8	107	2	S34005	Ig kappa chain V r
18	473.5	83.8	129	2	S40325	Ig kappa chain - h
19	470	83.2	129	2	S40363	Ig kappa chain - h
20	468.5	82.9	128	2	S40343	Ig kappa chain V-J
21	466	82.5	109	2	A30608	Ig kappa chain V-I
22	465	82.3	116	2	B26555	Ig kappa chain V-I
23	465	82.3	130	2	S40360	Ig kappa chain - h
24	465	82.3	215	2	JE0242	Ig kappa chain NIG
25	464	82.1	109	2	H30601	Ig kappa chain V-I
26	464	82.1	109	2	B30601	Ig kappa chain V-I
27	464	82.1	109	2	PH0963	Ig kappa chain V r
28	462	81.8	92	2	S37506	Ig kappa chain V r
29	462	81.8	108	2	C30608	Ig kappa chain V-I
30	462	81.8	109	2	G30607	Ig kappa chain V-I
31	462	81.8	109	2	F30607	Ig kappa chain V-I
32	461.5	81.7	108	2	E30609	Ig kappa chain V-I
33	461	81.6	92	2	S37516	Ig kappa chain V r
34	461	81.6	109	2	C30601	Ig kappa chain V-I
35	461	81.6	109	2	D30601	Ig kappa chain V-I
36	460	81.4	128	2	S20636	Ig kappa chain V r
37	460	81.4	129	1	K3HUHA	Ig kappa chain pre
38	459	81.2	109	1	K3HUPM	Ig kappa chain V-I
39	459	81.2	129	1	K3HUHI	Ig kappa chain pre
40	458	81.1	109	2	G30601	Ig kappa chain V-I
41	458	81.1	129	2	S46369	IG light chain var
42	458	81.1	131	2	S40328	Ig kappa chain - h
43	458	81.1	134	2	S38643	Ig kappa chain V r
44	454	80.4	108	2	B30608	Ig kappa chain V-I
45	454	80.4	109	1	K3HUSI	Ig kappa chain V-I
46	454	80.4	109	1	K3HUTI	Ig kappa chain V-I
47	453.5	80.3	110	2	E30607	Ig kappa chain V-I
48	453	80.2	129	2	S49532	anti-Sm antibody V
49	452	80.0	109	2	F30601	Ig kappa chain V-I
50	449	79.5	107	2	PH0965	Ig kappa chain V r
51	448	79.3	92	2	S37522	Ig kappa chain V r
52	448	79.3	109	1	K3HUWL	Ig kappa chain V-I
53	447.5	79.2	104	2	PH0964	Ig kappa chain V r
54	447	79.1	110	2	S20635	Ig kappa chain V r
55	447	79.1	111	2	PN0537	Ig kappa chain V r
56	446	78.9	86	2	S16826	Ig kappa chain V r
57	445.5	78.8	108	2	H44151	Ig kappa chain V r
58	445.5	78.8	215	2	JE0243	Ig kappa chain NIG
59	445	78.8	92	2	S37512	Ig kappa chain V r
60	444	78.6	86	2	S16833	Ig kappa chain V-I
61	443.5	78.5	110	2	S44120	Ig kappa chain V-J
62	443	78.4	215	2	A23746	Ig kappa chain V-I
63	442	78.2	121	2	S40327	Ig kappa chain - h
64	440	77.9	86	2	S16830	Ig kappa chain V r
65	440	77.9	127	2	S40380	Ig kappa chain V-J
66	439.5	77.8	123	2	S40378	Ig kappa chain - h
67	439	77.7	124	2	S20633	Ig kappa chain - h
68	439	77.7	129	2	A32274	Ig kappa chain pre
69	439	77.7	130	2	S20637	Ig kappa chain V r
70	437.5	77.4	128	1	K3HU41	Ig kappa chain pre
71	437	77.3	86	2	S16829	Ig kappa chain V r
72	437	77.3	109	2	F44151	Ig kappa chain V r
73	435.5	77.1	96	2	S45441	Ig kappa chain V r
74	435.5	77.1	119	2	S41816	Ig kappa chain V r
75	435	77.0	108	1	K3HUB6	Ig kappa chain V-I
76	434.5	76.9	131	2	S40346	Ig kappa chain V-J
77	434	76.8	86	2	S16837	Ig kappa chain V r
78	429.5	76.0	91	2	S37521	Ig kappa chain V r
79	429.5	76.0	107	2	S36264	Ig lambda chain V
80	429	75.9	92	2	S37504	Ig kappa chain V r
81	429	75.9	109	1	K3HUGO	Ig kappa chain V-I
82	428	75.8	115	1	K3HUCL	Ig kappa chain pre
83	427	75.6	98	2	I30608	Ig kappa chain V-I
84	427	75.6	115	2	A30553	Ig kappa chain pre
85	426.5	75.5	116	2	S41817	Ig kappa chain V r
86	426	75.4	86	2	S16834	Ig kappa chain V r
87	425.5	75.3	96	2	A30601	Ig kappa chain V-I
88	425.5	75.3	116	2	B27594	Ig kappa chain pre
89	425	75.2	95	2	PH0868	Ig kappa chain V r
90	425	75.2	109	2	S47181	Ig kappa chain - h
91	425	75.2	118	2	T03036	Ig light chain - h
92	424	75.0	86	2	S16824	Ig kappa chain V r
93	423	74.9	110	2	S40326	Ig kappa chain V-J
94	423	74.9	145	2	S20631	Ig kappa chain - h
95	422.5	74.8	116	2	C27594	Ig kappa chain pre
96	422.5	74.8	116	2	B25521	Ig kappa chain pre
97	420.5	74.4	116	1	K3HUVH	Ig kappa chain pre
98	419	74.2	86	2	S16836	Ig kappa chain V r
99	419	74.2	108	2	S33988	Ig kappa chain V r
100	418	74.0	92	2	S37523	Ig kappa chain V r

ALIGNMENTS

RESULT 1
S54905
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S54905
R;Esposito, G.; Traboni, C.
submitted to the EMBL Data Library, November 1994
A;Description: Cloning and sequencing of cDNA coding for the variable domains of a human
A;Reference number: S54905
A;Accession: S54905
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-114 <ESP>
A;Cross-references: EMBL:X82934; NID:g809554; PIDN:CAA58108.1; PID:g809555
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 94.5%; Score 534; DB 2; Length 114;
Best Local Similarity 93.5%; Pred. No. 5.3e-39;
Matches 101; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
::|:||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db 1 DVVMTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASRRATGIPA 60

Qy 61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
|||||||||||||||||||||||||||||||||| ||| ||||:||
Db 61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPLTFGGGTKVEIK 108

RESULT 2
S23628
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S23628
R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from t
A;Reference number: S23623; MUID:92156804; PMID:1740665
A;Accession: S23628
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-111 <OLE>
A;Cross-references: EMBL:X59705; NID:g34022; PIDN:CAA42226.1; PID:g1335190
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 530.5; DB 2; Length 111;
Best Local Similarity 96.3%; Pred. No. 1e-38;
Matches 104; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy 61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
|||||||||||||||||||||||||||||||| |:||| ||||:||
Db 61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNW-PWTFGQGTKVEIK 107

RESULT 3
PL0106
Ig kappa chain precursor V-J-C region (LS1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0106
R;Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A;Title: Relationship of variable region genes expressed by a human B cell lymphoma secre
A;Reference number: PL0106; MUID:89235583; PMID:2541221
A;Accession: PL0106
A;Molecule type: mRNA
A;Residues: 1-144 <SIL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-115/Domain: V region <VRE>
F;36-110/Domain: immunoglobulin homology <IMM>
F;44-54/Region: complementarity-determining 1
F;70-76/Region: complementarity-determining 2
F;109-115/Region: complementarity-determining 3
F;116-127/Domain: J region <JRG>
F;128-144/Domain: C region (fragment) <CRE>

Query Match 93.0%; Score 525.5; DB 2; Length 144;
Best Local Similarity 95.4%; Pred. No. 3.5e-38;
Matches 103; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQRPGQAPRLLIYDASNRATGIPA 80

Qy 61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
|||||||||||||||||||||||||||||||| | ||| ||||:||
Db 81 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNW-PLTFGGGTKVEIK 127

RESULT 4
A56701
Ig kappa chain V region precursor (HuA) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000
C;Accession: A56701
R;Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat, E.A.
J. Biol. Chem. 270, 12457-12465, 1995
A;Title: Human and mouse monoclonal antibodies to blood group A substance, which are nea
A;Reference number: A56701; MUID:95279371; PMID:7759488
A;Accession: A56701
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-128 <NIC>
A;Cross-references: GB:L41174; NID:g762823; PIDN:AAA64877.1; PID:g762824
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 92.7%; Score 523.5; DB 2; Length 128;
Best Local Similarity 95.4%; Pred. No. 4.7e-38;
Matches 103; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80

Qy 61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
|||||||||||||||||||||||||||||||| :|| ||||:||
Db 81 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPR-SFGQGTKVEIK 127

RESULT 5
G44151
Ig kappa chain V region (JM-10) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C;Accession: G44151
R;Zebedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caothien, R.H.; Graff, R.; DeGraw, J.; Pyat
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
A;Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
A;Reference number: A44151; MUID:92228746; PMID:1373487

```
A;Accession: G44151
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-108 <ZEB>
A;Cross-references: GB:M88317; NID:g183968; PIDN:AAA35975.1; PID:g183969
A;Note: nucleotide translation not given
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>

  Query Match             91.8%;  Score 518.5;  DB 2;  Length 108;
  Best Local Similarity   96.2%;  Pred. No. 1.1e-37;
  Matches  101;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          4 LTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFS 63
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 LTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFS 62

Qy         64 GSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||||| :|| ||||:||
Db         63 GSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPP-SFGGGTKVEIK 106


RESULT 6
S40345
Ig kappa chain V-J-C region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40345
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40345
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-128 <KLE>
A;Cross-references: EMBL:X72455; NID:g441378; PIDN:CAA51123.1; PID:g441379
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;32-106/Domain: immunoglobulin homology <IMM>

  Query Match             91.1%;  Score 514.5;  DB 2;  Length 128;
  Best Local Similarity   91.7%;  Pred. No. 2.7e-37;
  Matches  100;  Conservative    3;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              |||||||||||||||:|||||||||||  ||||||||||||||||||||| ||||||||
Db         17 EIVLTQSPATLSLSPGDRATLSCRASQSVRIYLAWYQQKPGQAPRLLIYDAINRATGIPA 76

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPP-FTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||||||||  ||| ||||::|
Db         77 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPTLTFGGGTKVEVK 125


RESULT 7
S29627
Ig kappa chain V region (60.3 hybridoma) - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S34110; S29627
R;Walls, M.A.; Hsiao, K.; Harris, L.J.
Nucleic Acids Res. 21, 2921-2929, 1993
A;Title: Vectors for the expression of PCR-amplified immunoglobulin variable domains wit
A;Reference number: S34110; MUID:93324379; PMID:8332501
A;Accession: S34110
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-129 <WA2>
A;Cross-references: EMBL:Z17330; NID:g38511; PIDN:CAA78978.1; PID:g38512
A;Note: human sequences cloned and sequenced prior to expression in mouse myeloma cells
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992
C;Genetics:
A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

  Query Match             90.9%;  Score 513.5;  DB 2;  Length 129;
  Best Local Similarity   92.7%;  Pred. No. 3.4e-37;
  Matches  101;  Conservative    1;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              |||||||||||||||||||||||||||||| |||||||||||||| ||||||||||||||
Db         21 EIVLTQSPATLSLSPGERATLSCRASQSVGSYLAWYQQKPGQAPRPLIYDASNRATGIPA 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPP-FTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||| | ||||  ||| ||||:||
Db         81 RFSGSGSGTDFTLTISSLEPEDFAVYYCQHRDNWPPGATFGGGTKVEIK 129


RESULT 8
S40379
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40379
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40379
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-128 <KLE>
A;Cross-references: EMBL:X72489; NID:g441446; PIDN:CAA51157.1; PID:g441447
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

  Query Match             89.1%;  Score 503.5;  DB 2;  Length 128;
  Best Local Similarity   91.7%;  Pred. No. 2.4e-36;
  Matches   99;  Conservative    3;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              | |||||:|||||||||||||||||||||||||||||||||||||| ||||||||||||
Db         21 EFVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQPPRLLIYYASNRATGIPA 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||:|||||||||||||||||||||||| | |:||| ||||:||
Db         81 RFSGSGAGTDFTLTISSLEPEDFAVYYCQQRSKW-PWTFGQGTKVEIK 127


RESULT 9
S57444
Ig kappa chain V-J region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 21-Jan-2000
C;Accession: S57444
R;Paterson, G.; Wilson, G.; Kennedy, P.G.E.; Willison, H.J.
submitted to the EMBL Data Library, June 1995
A;Description: Analysis of anti-GM1 ganglioside IgM antibodies cloned from motor neuropat
A;Reference number: S57408
A;Accession: S57444
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <PAT>
A;Cross-references: EMBL:X87898; NID:g871275; PIDN:CAA61149.1; PID:g871276
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             88.6%;  Score 500.5;  DB 2;  Length 107;
  Best Local Similarity   90.7%;  Pred. No. 3.6e-36;
  Matches   98;  Conservative    3;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
```

```
                  ||||||||||||||||||||||||||||||:||||||||||:| |||||||||| || |
Db          1 EIVLTQSPATLSLSPGERATLSCRASQSVSTYLAWYQQKPGQSPSLLIYDASNRAAGIAA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||||||||||||| ||| || |: |
Db         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPP-TFGQGTNVESK 107
```

RESULT 10
S40344
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40344
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40344
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-125 <KLE>
A;Cross-references: EMBL:X72454; NID:g441376; PIDN:CAA51122.1; PID:g441377
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

```
  Query Match             87.5%;  Score 494.5;  DB 2;  Length 125;
  Best Local Similarity   91.5%;  Pred. No. 1.4e-35;
  Matches   97;  Conservative    3;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              |:|||||||||||||||||||||||||||:||||||| ||||||||||||||||||||
Db         21 EVVLTQSPATLSLSPGERATLSCRASQSVSTYLAWYQQIPGQAPRLLIYDASNRATGIPA 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVD 106
              |||| |||||||||||||||||||||||| | | ||| ||||:
Db         81 RFSGRGSGTDFTLTISSLEPEDFAVYYCQQRSYW-PLTFGGGTKVE 125
```

RESULT 11
K3HUVG
Ig kappa chain precursor V-III region (Vg) - human
C;Species: Homo sapiens (man)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C;Accession: A01900
R;Pech, M.; Zachau, H.G.
Nucleic Acids Res. 12, 9229-9236, 1984
A;Title: Immunoglobulin genes of different subgroups are interdigitated within the V-K l
A;Reference number: A93549; MUID:85087932; PMID:6440122
A;Accession: A01900
A;Molecule type: DNA
A;Residues: 1-115 <PEC>
A;Cross-references: UNIPROT:P04433; GB:X01668; GB:K02768; NID:g33256; PIDN:CAB37836.1; P
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Gene: GDB:IGKV3
A;Cross-references: GDB:136266
A;Map position: 2p12-2p11
A;Introns: 17/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-115/Product: Ig kappa chain V-III region (Vg) #status predicted <MAT>
F;21-43/Region: framework 1
F;36-110/Domain: immunoglobulin homology <IMM>
F;44-54/Region: complementarity-determining 1
F;55-69/Region: framework 2
F;70-76/Region: complementarity-determining 2
F;77-108/Region: framework 3
F;109-115/Region: complementarity-determining 3
F;43-108/Disulfide bonds: #status predicted

```
  Query Match             87.3%;  Score 493;  DB 1;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-35;
  Matches   95;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWP 95
              |||||||||||||||||||||||||||||||||||
Db         81 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWP 115
```

RESULT 12
PC4282
Ig kappa chain (anti-SS-A/Ro 60K peptide) (E-42 and E-56) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000
C;Accession: PC4282; PC4284
R;Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H.
Biochem. Biophys. Res. Commun. 232, 101-106, 1997
A;Title: Molecular cloning of anti-ss-A/Ro 60-kDa peptide fab fragments from infiltrating
A;Reference number: PC4279; MUID:97236289; PMID:9125110
A;Accession: PC4282
A;Molecule type: protein
A;Residues: 1-106 <SUZ>
A;Note: E-42
A;Accession: PC4284
A;Molecule type: protein
A;Residues: 1-106 <SU2>
A;Note: E-56
C;Comment: This antibody is commonly found in systemic autoimmune diseases such as Sjoegr
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;14-88/Domain: immunoglobulin homology <IMM>

```
  Query Match             84.9%;  Score 479.5;  DB 2;  Length 106;
  Best Local Similarity   86.8%;  Pred. No. 2.3e-34;
  Matches   92;  Conservative    8;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          3 VLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF 62
              |||||||||||||||||||||||||:||||||||||||||||| | |||||||:|
Db          1 VLTQSPATLSLSPGERATLSCRASQSVSNYLAWYQQKPGQAPRLLIYDISKRATGIPAKF 60

Qy         63 SGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||:|||:||| |:|||||::| | ||| ||||:||
Db         61 SGSGSGTDFTLTVSSLQPEDSALYYCQQRASW-PLTFGGGTKVEIK 105
```

RESULT 13
S46375
Ig kappa chain V-J region (T33-5) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C;Accession: S46375; S38648
R;Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rea
A;Reference number: S46369; MUID:94313975; PMID:8039491
A;Accession: S46375
A;Molecule type: mRNA
A;Residues: 1-114 <BEN>
A;Cross-references: EMBL:Z27176; NID:g415967; PIDN:CAA81700.1; PID:g415968
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;20-95/Domain: immunoglobulin homology <IMM>

```
  Query Match             84.7%;  Score 478.5;  DB 2;  Length 114;
  Best Local Similarity   86.2%;  Pred. No. 2.9e-34;
  Matches   94;  Conservative    6;  Mismatches    8;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQKPGQAPRLLIYDASNRATGIP 59
```

```
                ||||||||| |||||||||||||||||||: |||||||||||||||||||| ||:||||||
Db          5 EIVLTQSPGTLSLSPGERATLSCRASQSISSSYLAWYQQKPGQAPRLLIYGASSRATGIP 64

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
                |||||||||||||||| ||||||||||||  : ||:||| |||::||
Db         65 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPPYTFGQGTKLEIK 113


RESULT 14
JE0244
Ig kappa chain NIG2 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0244
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T
submitted to JIPID, November 1998
A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A;Reference number: JE0243
A;Accession: JE0244
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             84.6%;  Score 478;  DB 2;  Length 215;
  Best Local Similarity   85.2%;  Pred. No. 5.9e-34;
  Matches   92;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              |:||||||||||:|||||||||||||||| | |||||||||||||||| || |||||||
Db          1 EVVLTQSPATLSVSPGERATLSCRASQSVHSNLAWYQQKPGQAPRLLIYRASTRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||| ||||||: ||||:||||| : ||| ||| |||||:||
Db         61 RFSGSGSGTDFILTISSLQSEDFALYYCQQYNTWPPLTFGGGTKVEIK 108


RESULT 15
S11697
Ig kappa chain precursor V-III region - human
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S11697
R;Pech, M.; Smola, H.; Pohlenz, H.D.; Straubinger, B.; Gerl, R.; Zachau, H.G.
J. Mol. Biol. 183, 291-299, 1985
A;Title: A large section of the gene locus encoding human immunoglobulin variable region
A;Reference number: S11697; MUID:85264787; PMID:3927006
A;Accession: S11697
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-115 <PEC>
A;Cross-references: EMBL:X17264; NID:g37898; PIDN:CAA35168.1; PID:g296688
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1989
C;Genetics:
A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

  Query Match             84.4%;  Score 477;  DB 2;  Length 115;
  Best Local Similarity   97.9%;  Pred. No. 4e-34;
  Matches   92;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db         21 EIVLTQSPATLSLSPGERATLSCRASQGVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNW 94
              ||||||| ||||||||||||||||||||||||||
Db         81 RFSGSGPGTDFTLTISSLEPEDFAVYYCQQRSNW 114


RESULT 16
S40362
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40362
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40362
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-117 <KLE>
A;Cross-references: EMBL:X72472; NID:g441412; PID:g441413
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;26-100/Domain: immunoglobulin homology <IMM>

  Query Match             84.3%;  Score 476.5;  DB 2;  Length 117;
  Best Local Similarity   87.0%;  Pred. No. 4.5e-34;
  Matches   94;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              |||:||||||||:|||||||||||||||| |||||||||||||||| || |||||||
Db         11 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 70

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||:||||||||: |||||||||| :|| | ||| ||||:||
Db         71 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNW-PLTFGGGTKVEIK 117


RESULT 17
S34005
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S34005; S30524
R;Mariette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A;Title: Nucleotidic sequence analysis of the variable domains of four human monoclonal
A;Reference number: S34001; MUID:93209281; PMID:7681398
A;Accession: S34005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <MAR>
A;Cross-references: EMBL:Z18330
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             83.8%;  Score 473.5;  DB 2;  Length 107;
  Best Local Similarity   87.0%;  Pred. No. 7.4e-34;
  Matches   94;  Conservative    5;  Mismatches    8;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              |||:||||||||:|||||||||||||||| |||||||||||||||| || |||||||
Db          1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||:||||||||: |||||||||| |||  ||| ||||:||
Db         61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYRNWPR-TFGQGTKVEIK 107


RESULT 18
S40325
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40325
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
```

```
A;Accession: S40325
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-129 <KLE>
A;Cross-references: EMBL:X72435; NID:g441338; PIDN:CAA51103.1; PID:g441339
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-110/Domain: immunoglobulin homology <IMM>

  Query Match             83.8%;  Score 473.5;  DB 2;  Length 129;
  Best Local Similarity   84.4%;  Pred. No. 8.9e-34;
  Matches   92;  Conservative    8;  Mismatches    8;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVS-SYLAWYQQKPGQAPRLLIYDASNRATGIP 59
              ::|||||| |||||||||||||||||||| ||||||||:|||||||||| ||:||||:|
Db         20 QLVLTQSPVTLSLSPGERATLSCRASQSVSGSYLAWYQQRPGQAPRLLIYGASSRATGVP 79

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
                |||||||||||||| :||||||||||  : | ||||||||||:
Db         80 DRFSGSGSGTDFTLTISRMEPEDFAVYYCQQYGSSPLFTFGPGTKVDIR 128


RESULT 19
S40363
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40363
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40363
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-129 <KLE>
A;Cross-references: EMBL:X72473; NID:g441414; PIDN:CAA51141.1; PID:g441415
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-109/Domain: immunoglobulin homology <IMM>

  Query Match             83.2%;  Score 470;  DB 2;  Length 129;
  Best Local Similarity   85.2%;  Pred. No. 1.8e-33;
  Matches   92;  Conservative    7;  Mismatches    7;  Indels    2;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||:|| |:|
Db         20 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASHRAPGVPT 79

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||||||||:||||:      |:|| |||::||
Db         80 RFSGSGSGTDFTLTISSLEPEDFAIYYCQRCKGM--FSFGQGTKLEIK 125


RESULT 20
S40343
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40343
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40343
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-128 <KLE>
A;Cross-references: EMBL:X72453; NID:g441374; PIDN:CAA51121.1; PID:g441375
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

  Query Match             82.9%;  Score 468.5;  DB 2;  Length 128;
  Best Local Similarity   84.3%;  Pred. No. 2.4e-33;
  Matches   91;  Conservative    9;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              |||:|||||||:|||||||||||||||||| |||||||||||| :||| || |||||||
Db         21 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPTVLIYGASTRATGIPA 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||:||||||||: |||||||||| :|| |:||| |||::||
Db         81 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNW-PYTFGQGTKLEIK 127


RESULT 21
A30608
Ig kappa chain V-III region (Son) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004
C;Accession: A30608
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solon
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantib
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: A30608
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON>
A;Cross-references: UNIPROT:Q9UL78
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

  Query Match             82.5%;  Score 466;  DB 2;  Length 109;
  Best Local Similarity   87.2%;  Pred. No. 3.3e-33;
  Matches   95;  Conservative    4;  Mismatches    8;  Indels    2;  Gaps    2;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQKPGQAPRLLIYDASNRATGIP 59
              |||||||| |||||||||||||||||||| |||||||||||||||||||| ||:||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||| ||||||||||||  :  |:||| ||||:||
Db         61 NRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS-SPYTFGGGTKVEIK 108


RESULT 22
B26555
Ig kappa chain V-III region (Ger) - human
C;Species: Homo sapiens (man)
C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000
C;Accession: B26555
R;Middaugh, C.R.; Litman, G.W.
J. Biol. Chem. 262, 3671-3673, 1987
A;Title: Atypical glycosylation of an IgG monoclonal cryoimmunoglobulin.
A;Reference number: A92630; MUID:87137666; PMID:3102493
A;Accession: B26555
A;Molecule type: protein
A;Residues: 1-116 <MID>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             82.3%;  Score 465;  DB 2;  Length 116;
  Best Local Similarity   81.5%;  Pred. No. 4.3e-33;
  Matches   88;  Conservative   10;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              :||:|| |||||:|||| |||||||||:|| |||||||||||||||| || |||||||
Db          1 DIVMTQVPATLSVSPGEGATLSCRASQSISSNLAWYQQKPGQAPRLLIYAASTRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||:||||||||: |||||||||| :||| ||| ||:::||
Db         61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYDDWPPITFGQGTRLEIK 108
```

RESULT 23
S40360
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40360
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40360
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-130 <KLE>
A;Cross-references: EMBL:X72470; NID:g441408; PIDN:CAA51138.1; PID:g441409
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-111/Domain: immunoglobulin homology <IMM>

Query Match 82.3%; Score 465; DB 2; Length 130;
Best Local Similarity 84.5%; Pred. No. 4.8e-33;
Matches 93; Conservative 3; Mismatches 12; Indels 2; Gaps 1;

```
Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVS--SYLAWYQQKPGQAPRLLIYDASNRATGI 58
              |||||||| |||||||||||||||||||||  : | |||||||||||||||||||||||
Db         20 EIVLTQSPGTLSLSPGERATLSCRASQSVSYNNNLGWYQQKPGQAPRLLIYDASNRATGI 79

Qy         59 PARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              | ||||||||||||||| |||:||||||||     || ||| ||||:||
Db         80 PDRFSGSGSGTDFTLTISRLEPQDFAVYYCQHYGRSPPLTFGGGTKVEIK 129
```

RESULT 24
JE0242
Ig kappa chain NIG26 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0242
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T
submitted to JIPID, November 1998
A;Description: Structure relationship of kappatype light chains with AL amyloidosis: Mul
A;Reference number: JE0241
A;Accession: JE0242
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 82.3%; Score 465; DB 2; Length 215;
Best Local Similarity 86.2%; Pred. No. 7.7e-33;
Matches 94; Conservative 4; Mismatches 9; Indels 2; Gaps 2;

```
Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVS-SYLAWYQQKPGQAPRLLIYDASNRATGIP 59
              |||||||| |||||||||||||||||||| :|||||||||||| |||||||:||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSNNYLAWYQQKPGQAPSLLIYDASSRATGIP 60

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||| |||| ||||||||||||||    ||:||| ||||:||
Db         61 DRFSGSGSGTDFILTISGLEPEDFAVYYCQQYDR-PPWTFGQGTKVEIK 108
```

RESULT 25
H30601
Ig kappa chain V-III region (Gar and Flo) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C;Accession: H30601; E30601
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc
J. Immunol. 142; 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: H30601
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON1>
A;Accession: E30601
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-109 <GON2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 82.1%; Score 464; DB 2; Length 109;
Best Local Similarity 86.2%; Pred. No. 4.9e-33;
Matches 94; Conservative 5; Mismatches 8; Indels 2; Gaps 2;

```
Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQKPGQAPRLLIYDASNRATGIP 59
              |||||||| |||||||||||||||||||| |||||||||||||||||||| ||:||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||| |||||||||||||  :  |:||| |||::||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS-SPYTFGQGTKLEIK 108
```

Search completed: June 16, 2005, 07:44:57
Job time : 22.7623 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2005, 07:35:00 ; Search time 108.484 Seconds
(without alignments)
509.793 Million cell updates/sec

Title: US-09-920-137D-8
Perfect score: 565
Sequence: 1 EIVLTQSPATLSLSPGERAT.....QQRSNWPPFTFGPGTKVDIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	493	87.3	115	1	KV3I_HUMAN	P04433 homo sapien
2	485.5	85.9	108	2	Q9UL83	Q9ul83 homo sapien
3	480	85.0	129	1	KV3H_HUMAN	P04207 homo sapien
4	474	83.9	109	2	Q9UL85	Q9ul85 homo sapien
5	460	81.4	129	1	KV3L_HUMAN	P18135 homo sapien
6	459	81.2	109	1	KV3F_HUMAN	P01624 homo sapien
7	459	81.2	129	1	KV3M_HUMAN	P18136 homo sapien
8	455	80.5	109	2	Q9UL78	Q9ul78 homo sapien
9	454	80.4	109	1	KV3B_HUMAN	P01620 homo sapien
10	454	80.4	109	1	KV3D_HUMAN	P01622 homo sapien
11	454	80.4	109	2	Q9UL86	Q9ul86 homo sapien
12	453.5	80.3	236	2	Q6PIL8	Q6pil8 homo sapien
13	453	80.2	235	2	Q6PJF2	Q6pjf2 homo sapien
14	448	79.3	109	1	KV3E_HUMAN	P01623 homo sapien
15	448	79.3	235	2	Q6GMW0	Q6gmw0 homo sapien
16	444.5	78.7	236	2	Q6P5S8	Q6p5s8 homo sapien
17	437.5	77.4	128	1	KV3K_HUMAN	P06311 homo sapien
18	435	77.0	108	1	KV3A_HUMAN	P01619 homo sapien
19	431	76.3	235	2	Q6GMV9	Q6gmv9 homo sapien
20	429	75.9	109	1	KV3G_HUMAN	P04206 homo sapien
21	420.5	74.4	116	1	KV3J_HUMAN	P04434 homo sapien
22	417.5	73.9	100	1	KV3C_HUMAN	P01621 homo sapien
23	417.5	73.9	236	2	Q6GMX8	Q6gmx8 homo sapien
24	410.5	72.7	108	1	KV1M_HUMAN	P01605 homo sapien
25	404	71.5	107	1	KV1D_HUMAN	P01596 homo sapien
26	402.5	71.2	236	2	Q6PIH7	Q6pih7 homo sapien
27	399.5	70.7	108	2	Q9UL79	Q9ul79 homo sapien
28	398	70.4	107	2	Q96SA9	Q96sa9 homo sapien
29	396.5	70.2	108	2	Q9UL77	Q9ul77 homo sapien
30	392.5	69.5	244	2	Q65ZC8	Q65zc8 homo sapien
31	391.5	69.3	108	1	KV1H_HUMAN	P01600 homo sapien
32	391	69.2	107	2	Q9UL81	Q9ul81 homo sapien
33	388.5	68.8	108	1	KV1V_HUMAN	P04430 homo sapien
34	388.5	68.8	240	2	Q65ZC9	Q65zc9 homo sapien
35	387.5	68.6	111	1	KV3M_MOUSE	P01665 mus musculu
36	386.5	68.4	236	2	Q6GMW1	Q6gmw1 homo sapien
37	385.5	68.2	108	2	Q9UL70	Q9ul70 homo sapien
38	384.5	68.1	108	1	KV1L_HUMAN	P01604 homo sapien
39	383.5	67.9	111	1	KV3O_MOUSE	P01667 mus musculu
40	383.5	67.9	134	1	KV4C_HUMAN	P06314 homo sapien
41	382.5	67.7	236	2	Q6PIT5	Q6pit5 homo sapien
42	381.5	67.5	108	1	KV1K_HUMAN	P01603 homo sapien
43	380.5	67.3	108	1	KV1E_HUMAN	P01597 homo sapien
44	380.5	67.3	108	1	KV1P_HUMAN	P01608 homo sapien
45	380.5	67.3	111	1	KV3H_MOUSE	P01660 mus musculu
46	380.5	67.3	111	1	KV3L_MOUSE	P01664 mus musculu
47	379.5	67.2	108	1	KV1B_HUMAN	P01594 homo sapien
48	379.5	67.2	111	1	KV3N_MOUSE	P01666 mus musculu
49	378	66.9	112	1	KV3B_MOUSE	P01655 mus musculu
50	377	66.7	133	1	KV4B_HUMAN	P06313 homo sapien
51	376.5	66.6	108	1	KV1Y_HUMAN	P80362 homo sapien
52	376.5	66.6	236	2	Q6GMX0	Q6gmx0 homo sapien
53	375.5	66.5	111	1	KV3Q_MOUSE	P01669 mus musculu
54	375.5	66.5	114	1	KV4A_HUMAN	P01625 homo sapien
55	375.5	66.5	131	2	Q811C3	Q811c3 mus musculu
56	375.5	66.5	234	2	Q7Z473	Q7z473 homo sapien
57	375.5	66.5	236	2	Q6GMX9	Q6gmx9 homo sapien
58	375.5	66.5	236	2	Q6PIH4	Q6pih4 homo sapien
59	375.5	66.5	236	2	Q7Z3Y4	Q7z3y4 homo sapien
60	373.5	66.1	108	1	KV1S_HUMAN	P01611 homo sapien
61	373.5	66.1	129	1	KV1X_HUMAN	P04432 homo sapien
62	372	65.8	109	1	KV1T_HUMAN	P01612 homo sapien
63	371.5	65.8	108	1	KV1F_HUMAN	P01598 homo sapien
64	370.5	65.6	111	1	KV3J_MOUSE	P01662 mus musculu
65	370.5	65.6	111	2	Q920E9	Q920e9 mus musculu
66	370.5	65.6	116	2	Q96PF6	Q96pf6 homo sapien
67	370	65.5	117	1	KV1J_HUMAN	P01602 homo sapien
68	369.5	65.4	108	1	KV1N_HUMAN	P01606 homo sapien
69	368.5	65.2	111	1	KV3T_MOUSE	P01672 mus musculu
70	368.5	65.2	129	1	KV1W_HUMAN	P04431 homo sapien
71	368.5	65.2	131	1	KV3I_MOUSE	P01661 mus musculu
72	368	65.1	110	1	KV3P_MOUSE	P01668 mus musculu
73	366.5	64.9	108	1	KV1O_HUMAN	P01607 homo sapien
74	366.5	64.9	111	1	KV3K_MOUSE	P01663 mus musculu
75	366.5	64.9	111	1	KV3S_MOUSE	P01671 mus musculu
76	366.5	64.9	111	2	Q811U6	Q811u6 mus musculu
77	366	64.8	112	2	Q8K1F2	Q8k1f2 mus musculu
78	365.5	64.7	108	1	KV1G_HUMAN	P01599 homo sapien
79	365.5	64.7	108	1	KV1R_HUMAN	P01610 homo sapien
80	365.5	64.7	111	1	KV3U_MOUSE	P01673 mus musculu
81	365.5	64.7	255	2	Q6KB05	Q6kb05 mus musculu
82	365.5	64.7	262	2	Q65ZI1	Q65zi1 mus musculu
83	365	64.6	114	2	Q8K1F1	Q8k1f1 mus musculu
84	364.5	64.5	111	1	KV3R_MOUSE	P01670 mus musculu
85	364	64.4	111	2	Q65ZN3	Q65zn3 mus musculu
86	364	64.4	134	2	Q8VDD0	Q8vdd0 mus musculu
87	363.5	64.3	111	1	KV3D_MOUSE	P03977 mus musculu
88	363.5	64.3	149	1	KV5A_MOUSE	P01633 mus musculu
89	363.5	64.3	240	2	Q6PIH6	Q6pih6 homo sapien
90	362.5	64.2	108	1	KV1C_HUMAN	P01595 homo sapien
91	362	64.1	108	1	KV6K_MOUSE	P04945 mus musculu
92	361.5	64.0	108	1	KV1Q_HUMAN	P01609 homo sapien
93	361.5	64.0	111	1	KV3A_MOUSE	P01654 mus musculu
94	361.5	64.0	238	2	Q66JS7	Q66js7 mus musculu
95	361	63.9	106	2	Q9U410	Q9u410 schistosoma
96	361	63.9	112	2	Q8K1F3	Q8k1f3 mus musculu
97	360.5	63.8	108	1	KV1A_HUMAN	P01593 homo sapien
98	360.5	63.8	111	1	KV3C_MOUSE	P01656 mus musculu
99	359.5	63.6	136	1	KV5B_MOUSE	P01634 mus musculu
100	357.5	63.3	114	2	Q9UL80	Q9ul80 homo sapien

ALIGNMENTS

```
RESULT 1
KV3I_HUMAN
ID   KV3I_HUMAN     STANDARD;      PRT;   115 AA.
AC   P04433;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region VG precursor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85087932; PubMed=6440122;
RA   Pech M., Zachau H.G.;
RT   "Immunoglobulin genes of different subgroups are interdigitated within
RT   the VK locus.";
RL   Nucleic Acids Res. 12:9229-9236(1984).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X01668; -; NOT_ANNOTATED_CDS.
DR   PIR; A01900; K3HUVG.
DR   HSSP; P01625; 1EEQ.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21   >115       Ig kappa chain V-III region VG.
FT   DOMAIN       21     43       Framework-1.
FT   DOMAIN       44     54       Complementarity-determining-1.
FT   DOMAIN       55     69       Framework-2.
FT   DOMAIN       70     76       Complementarity-determining-2.
FT   DOMAIN       77    108       Framework-3.
FT   DOMAIN      109    115       Complementarity-determining-3.
FT   DISULFID     43    108       By similarity.
FT   NON_TER     115    115
SQ   SEQUENCE   115 AA;  12575 MW;  2DE47CDA3A17D555 CRC64;

  Query Match             87.3%;  Score 493;  DB 1;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-42;
  Matches   95;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWP 95
              |||||||||||||||||||||||||||||||||||
Db         81 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWP 115


RESULT 2
Q9UL83
ID   Q9UL83      PRELIMINARY;      PRT;   108 AA.
AC   Q9UL83;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035031; AAD56267.1; -.
DR   PIR; B30609; B30609.
DR   PIR; C30609; C30609.
DR   PIR; D30609; D30609.
DR   PIR; S34098; S34098.
DR   PIR; S34099; S34099.
DR   HSSP; P01625; 1LVE.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11834 MW;  9F9C5A92EBA96EEA CRC64;

  Query Match             85.9%;  Score 485.5;  DB 2;  Length 108;
  Best Local Similarity   88.9%;  Pred. No. 1.4e-41;
  Matches   96;  Conservative    5;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              |||:||||||||:||||||||||||||||||| |||||||||||||||| || |||||||
Db          1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYCASTRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||:||||||||: |||||||||  :|| ||||||||||||||
Db         61 RFSGSGSGTEFTLTISSLQFEDFAVYYCQHYNNW-PFTFGPGTKVDIK 107


RESULT 3
KV3H_HUMAN
ID   KV3H_HUMAN     STANDARD;      PRT;   129 AA.
AC   P04207;
DT   20-MAR-1987 (Rel. 04, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86177570; PubMed=3083417;
RA   Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
RA   Goldfien R., Carson D.A.;
RT   "Cloning and sequence determination of a human rheumatoid factor
RT   light-chain gene.";
RL   Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M12740; AAA58992.1; -.
DR   HSSP; P01625; 1LVE.
```

```
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     20
FT   CHAIN       21    129       Ig kappa chain V-III region CLL.
FT   DOMAIN      21     43       Framework-1.
FT   DOMAIN      44     54       Complementarity-determining-1.
FT   DOMAIN      55     69       Framework-2.
FT   DOMAIN      70     76       Complementarity-determining-2.
FT   DOMAIN      77    108       Framework-3.
FT   DOMAIN     109    118       Complementarity-determining-3.
FT   DOMAIN     119    129       JK1 segment.
FT   DISULFID    43    108       By similarity.
FT   NON_TER    129    129
SQ   SEQUENCE   129 AA;  14275 MW;  5C13B411BE60CC14 CRC64;

  Query Match             85.0%;  Score 480;  DB 1;  Length 129;
  Best Local Similarity   84.3%;  Pred. No. 6e-41;
  Matches   91;  Conservative    9;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              |||:||||||||:||||||||||||||||||: |||||||||| |||||| || |||||||
Db         21 EIVMTQSPATLSVSPGERATLSCRASQSVSNNLAWYQQKPGQPPRLLIYGASTRATGIPA 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||:|||||| |: |||||||||| :||||:||| ||:|:||
Db         81 RFSGSGSGTEFTLTISRLQSEDFAVYYCQQYNNWPPWTFGQGTRVEIK 128


RESULT 4
Q9UL85
ID   Q9UL85      PRELIMINARY;      PRT;   109 AA.
AC   Q9UL85;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin kappa chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035029; AAD56265.1; -.
DR   PIR; D30609; D30609.
DR   HSSP; P01625; 1EK3.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER      1      1
FT   NON_TER    109    109
SQ   SEQUENCE   109 AA;  11761 MW;  FB1E43E7C7AFACCC CRC64;

  Query Match             83.9%;  Score 474;  DB 2;  Length 109;
  Best Local Similarity   83.3%;  Pred. No. 2e-40;
  Matches   90;  Conservative   10;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              |||:||||||||:|||||||||| ||||:|| |||||||||||||||| || |||||||
Db          1 EIVMTQSPATLSVSPGERATLSCWASQSISSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||:|||||||: |||||:|:||| ::||| ||| ||||:||
Db         61 RFSGSGSGTEFTLTISSLQSEDFAIYHCQQYNSWPPLTFGGGTKVEIK 108


RESULT 5
KV3L_HUMAN
ID   KV3L_HUMAN     STANDARD;      PRT;   129 AA.
AC   P18135;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region HAH precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88171307; PubMed=3127527;
RA   Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT   "Autoantibody-associated kappa light chain variable region gene
RT   expressed in chronic lymphocytic leukemia with little or no somatic
RT   mutation. Implications for etiology and immunotherapy.";
RL   J. Exp. Med. 167:840-852(1988).
CC   -!- DISEASE: The protein is one of the surface immunoglobulin M
CC       autoantibodies expressed in patients with chronic lymphocytic
CC       leukemia.
DR   PIR; PL0022; K3HUHA.
DR   HSSP; P01625; 1EEQ.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     20
FT   CHAIN       21    129       Ig kappa chain V-III region HAH.
FT   DOMAIN      21     43       Framework-1.
FT   DOMAIN      44     55       Complementarity-determining-1.
FT   DOMAIN      56     70       Framework-2.
FT   DOMAIN      71     77       Complementarity-determining-2.
FT   DOMAIN      78    109       Framework-3.
FT   DOMAIN     110    118       Complementarity-determining-3.
FT   DOMAIN     119    129       JK1 segment.
FT   DISULFID    43    109       By similarity.
FT   NON_TER    129    129
SQ   SEQUENCE   129 AA;  14073 MW;  D3C55292772774D0 CRC64;

  Query Match             81.4%;  Score 460;  DB 1;  Length 129;
  Best Local Similarity   87.2%;  Pred. No. 6.5e-39;
  Matches   95;  Conservative    2;  Mismatches   10;  Indels    2;  Gaps    2;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQKPGQAPRLLIYDASNRATGIP 59
              |||||||| |||||||||||||||||||| |||||||||||||||||| ||:|||||||
Db         21 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 80

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||| ||||||||||||     | ||| ||||:||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGT-SPRTFGQGTKVEIK 128


RESULT 6
KV3F_HUMAN
ID   KV3F_HUMAN     STANDARD;      PRT;   109 AA.
AC   P01624;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
```

```
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-III region POM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76276460; PubMed=60899;
RA   Klapper D.G., Capra J.D.;
RT   "The amino acid sequence of the variable regions of the light chains
RT   from two idiotypically cross reactive IgM anti-gamma globulins.";
RL   Ann. Immunol. (Paris) 127C:261-271(1976).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC       globulin activity.
DR   PIR; A01897; K3HUPM.
DR   HSSP; P01625; 1LVE.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DISULFID     23     89       By similarity.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11922 MW;  62821DDC6A8ABA86 CRC64;

  Query Match             81.2%;  Score 459;  DB 1;  Length 109;
  Best Local Similarity   82.6%;  Pred. No. 6.7e-39;
  Matches   90;  Conservative    9;  Mismatches    8;  Indels    2;  Gaps    2;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVS-SYLAWYQQKPGQAPRLLIYDASNRATGIP 59
              |||:|||| |||:|||||||||||||||:| |||||||||| :|||||| || ||||||
Db          1 EIVMTQSPVTLSVSPGERATLSCRASQSISNSYLAWYQQKPSGSPRLLIYGASTRATGIP 60

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||:||||||||: |||||||||| :|||| ||| ||:|:||
Db         61 ARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPP-TFGQGTRVEIK 108


RESULT 7
KV3M_HUMAN
ID   KV3M_HUMAN     STANDARD;      PRT;   129 AA.
AC   P18136;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region HIC precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88171307; PubMed=3127527;
RA   Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT   "Autoantibody-associated kappa light chain variable region gene
RT   expressed in chronic lymphocytic leukemia with little or no somatic
RT   mutation. Implications for etiology and immunotherapy.";
RL   J. Exp. Med. 167:840-852(1988).
CC   -!- DISEASE: The protein is one of the surface immunoglobulin M
CC       autoantibodies expressed in patients with chronic lymphocytic
CC       leukemia.
DR   PIR; PL0021; K3HUHI.
DR   HSSP; P01625; 1EEQ.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    129       Ig kappa chain V-III region HIC.
FT   DOMAIN       21     43       Framework-1.
FT   DOMAIN       44     55       Complementarity-determining-1.
FT   DOMAIN       56     70       Framework-2.
FT   DOMAIN       71     77       Complementarity-determining-2.
FT   DOMAIN       78    109       Framework-3.
FT   DOMAIN      110    118       Complementarity-determining-3.
FT   DOMAIN      119    129       JK1 segment.
FT   DISULFID     43    109       By similarity.
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  14070 MW;  7395528EA2BB74D6 CRC64;

  Query Match             81.2%;  Score 459;  DB 1;  Length 129;
  Best Local Similarity   86.2%;  Pred. No. 8.2e-39;
  Matches   94;  Conservative    4;  Mismatches    9;  Indels    2;  Gaps    2;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQKPGQAPRLLIYDASNRATGIP 59
              |||||||| |||||||||||||||||||| |||||||||||||||||| ||:||||||
Db         21 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 80

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||| ||| |||||||||  :  |:||| ||||:||
Db         81 DRFSGSGSGTDFTLTISRLEPXDFAVYYCQQYGS-SPWTFGQGTKVEIK 128


RESULT 8
Q9UL78
ID   Q9UL78      PRELIMINARY;      PRT;   109 AA.
AC   Q9UL78;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035036; AAD56272.1; -.
DR   PIR; A30601; A30601.
DR   PIR; A30608; A30608.
DR   PIR; B30601; B30601.
DR   PIR; B30607; B30607.
DR   PIR; C30601; C30601.
DR   PIR; C30607; C30607.
DR   PIR; C30608; C30608.
DR   PIR; D30601; D30601.
DR   PIR; D30607; D30607.
DR   PIR; D30608; D30608.
DR   PIR; F30607; F30607.
DR   PIR; F30608; F30608.
DR   PIR; G30601; G30601.
DR   PIR; G30608; G30608.
DR   PIR; H30607; H30607.
DR   PIR; H30608; H30608.
DR   PIR; H44151; H44151.
DR   PIR; I30601; I30601.
DR   PIR; PH0963; PH0963.
DR   PIR; PH0964; PH0964.
DR   PIR; PH0965; PH0965.
```

```
DR   PIR; S33988; S33988.
DR   PIR; S34096; S34096.
DR   HSSP; P01625; 1EK3.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11646 MW;  5F675C52EC7EE197 CRC64;

  Query Match             80.5%;  Score 455;  DB 2;  Length 109;
  Best Local Similarity   86.2%;  Pred. No. 1.7e-38;
  Matches   94;  Conservative    3;  Mismatches   10;  Indels    2;  Gaps    2;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQKPGQAPRLLIYDASNRATGIP 59
              |||||||| |||||||||||||||||||| |||||||||||||||||||| ||:||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||| ||||| |||||||   :  | ||| ||||:||
Db         61 DRFSGSGSGTDFTLTISRLEPEDCAVYYCQQYGS-SPLTFGGGTKVEIK 108


RESULT 9
KV3B_HUMAN
ID   KV3B_HUMAN     STANDARD;      PRT;   109 AA.
AC   P01620;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-III region SIE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=82046598; PubMed=6794615;
RA   Andrews D.W., Capra J.D.;
RT   "Amino acid sequence of the variable regions of light chains from two
RT   idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT   group.";
RL   Biochemistry 20:5816-5822(1981).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC       globulin activity.
DR   PIR; A01892; K3HUSI.
DR   HSSP; P01625; 1LVE.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DISULFID     23     89       By similarity.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11775 MW;  7689C3ECD646FFB4 CRC64;

  Query Match             80.4%;  Score 454;  DB 1;  Length 109;
  Best Local Similarity   85.3%;  Pred. No. 2.2e-38;
  Matches   93;  Conservative    5;  Mismatches    9;  Indels    2;  Gaps    2;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVS-SYLAWYQQKPGQAPRLLIYDASNRATGIP 59
              |||||||| |||||||||||||||||||| |||||||||||||||||||| ||:||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSNSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||| ||||:||||||||  :  | ||| |:||:||
Db         61 DRFSGSGSGTDFTLTISRLEPDDFAVYYCQQYGS-SPQTFGQGSKVEIK 108


RESULT 10
KV3D_HUMAN
ID   KV3D_HUMAN     STANDARD;      PRT;   109 AA.
AC   P01622;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-III region Ti.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72188439; PubMed=5027703;
RA   Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT   Ti). IV. The complete amino acid sequence and its significance for the
RT   mechanism of antibody production.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A01895; K3HUTI.
DR   HSSP; P01625; 1LVE.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin V region.
FT   DISULFID     23     89       By similarity.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11788 MW;  8C35058CDC7749BC CRC64;

  Query Match             80.4%;  Score 454;  DB 1;  Length 109;
  Best Local Similarity   85.3%;  Pred. No. 2.2e-38;
  Matches   93;  Conservative    5;  Mismatches    9;  Indels    2;  Gaps    2;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVS-SYLAWYQQKPGQAPRLLIYDASNRATGIP 59
              |||||||| |||||||||||||||||||| |:||||||||||||||||||| ||:||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSNSFLAWYQQKPGQAPRLLIYVASSRATGIP 60

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||||| ||||||||||||  :  | ||| ||||::|
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS-SPSTFGQGTKVELK 108


RESULT 11
Q9UL86
ID   Q9UL86      PRELIMINARY;      PRT;   109 AA.
AC   Q9UL86;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin kappa chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
```

```
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035028; AAD56264.1; -.
DR   PIR; B30607; B30607.
DR   PIR; I30601; I30601.
DR   HSSP; P01625; 1EK3.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11928 MW;  243325F72C7DAC83 CRC64;

  Query Match             80.4%;  Score 454;  DB 2;  Length 109;
  Best Local Similarity   86.2%;  Pred. No. 2.2e-38;
  Matches   94;  Conservative    2;  Mismatches   11;  Indels    2;  Gaps    2;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQKPGQAPRLLIYDASNRATGIP 59
              |||||||| |||| |||||||||||||| |||||||||||||||||||  |:||||||
Db          1 EIVLTQSPGTLSLFPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIP 60

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
               ||||||| |||||||| |||||||||||||  :   ||||||||||||
Db         61 DRFSGSGSETDFTLTISRLEPEDFAVYYCQQYGS-SIFTFGPGTKVDIK 108


RESULT 12
Q6PIL8
ID   Q6PIL8      PRELIMINARY;      PRT;   236 AA.
AC   Q6PIL8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC032451; AAH32451.1; -.
DR   HSSP; P01837; 1KCU.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25834 MW;  6647A9E77A3C0053 CRC64;

  Query Match             80.3%;  Score 453.5;  DB 2;  Length 236;
  Best Local Similarity   83.5%;  Pred. No. 6e-38;
  Matches   91;  Conservative    4;  Mismatches   13;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQKPGQAPRLLIYDASNRATGIP 59
              | |||||| ||||||||||||||||||: |||||||||||||||||||  |:||||||
Db         21 ENVLTQSPGTLSLSPGERATLSCRASQSLSSSYLAWYQQKPGQAPRLLIYGVSSRATGIP 80

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
               |||||||||||||| ||||||||||||     | ||| ||::|||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSRPITFGQGTRLDIK 129


RESULT 13
Q6PJF2
ID   Q6PJF2      PRELIMINARY;      PRT;   235 AA.
AC   Q6PJF2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC016380; AAH16380.1; -.
DR   HSSP; P01837; 1KCU.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
```

```
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   235 AA;  25520 MW;  F33A145A396BA285 CRC64;

  Query Match             80.2%;  Score 453;  DB 2;  Length 235;
  Best Local Similarity   85.3%;  Pred. No. 6.7e-38;
  Matches   93;  Conservative    5;  Mismatches    9;  Indels    2;  Gaps    2;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSS-YLAWYQQKPGQAPRLLIYDASNRATGIP 59
              |||||||||||||||||||||||||||| ||| |||||||||||||||:: :|:||||||
Db         21 EIVLTQSPATLSLSPGERATLSCRASQIVSSAYLAWYQQKPGQAPRLLMFGSSSRATGIP 80

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
                |||||||||||||||| ||||||||||||  :    ||||||||||
Db         81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS-SQGTFGPGTKVDIK 128


RESULT 14
KV3E_HUMAN
ID   KV3E_HUMAN     STANDARD;      PRT;   109 AA.
AC   P01623;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-III region WOL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=82046598; PubMed=6794615;
RA   Andrews D.W., Capra J.D.;
RT   "Amino acid sequence of the variable regions of light chains from two
RT   idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT   group.";
RL   Biochemistry 20:5816-5822(1981).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC       globulin activity.
DR   PIR; A01896; K3HUWL.
DR   HSSP; P01625; 1LVE.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DISULFID     23     89       By similarity.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11746 MW;  566C115E6B9CBEEE CRC64;

  Query Match             79.3%;  Score 448;  DB 1;  Length 109;
  Best Local Similarity   85.3%;  Pred. No. 8.8e-38;
  Matches   93;  Conservative    3;  Mismatches   11;  Indels    2;  Gaps    2;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSS-YLAWYQQKPGQAPRLLIYDASNRATGIP 59
              |||||||| |||||||||||||||||||||| || |||||||||||||||| ||:||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSGYLGWYQQKPGQAPRLLIYGASSRATGIP 60

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
                |||||||||||||||| ||||||||||||  :    ||| ||||:||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSLGR-TFGQGTKVEIK 108


RESULT 15
Q6GMW0
ID   Q6GMW0      PRELIMINARY;      PRT;   235 AA.
AC   Q6GMW0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073792; AAH73792.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   235 AA;  25765 MW;  4360C36B6D4133F5 CRC64;

  Query Match             79.3%;  Score 448;  DB 2;  Length 235;
  Best Local Similarity   77.8%;  Pred. No. 2.2e-37;
  Matches   84;  Conservative   15;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              |||:||||||||:||||||||||||||||:|: ||||||:|||||||||| ||:| ||||
Db         21 EIVMTQSPATLSVSPGERATLSCRASQSISNNLAWYQQRPGQAPRLLIYGASSRVTGIPG 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||:|||:||||: ||||||:||| ::|  :||| |||::||
Db         81 RFSGSGSGTEFTLSISSLQSEDFAVYFCQQYNDWLLYTFGQGTKLEIK 128


RESULT 16
Q6P5S8
ID   Q6P5S8      PRELIMINARY;      PRT;   236 AA.
AC   Q6P5S8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
```

```
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Glandular pool- thyroid;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Glandular pool- thyroid;
RA   Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC062704; AAH62704.1; -.
DR   HSSP; P01837; 1KCU.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25773 MW;  953E37BEB4FF5F27 CRC64;

  Query Match             78.7%;  Score 444.5;  DB 2;  Length 236;
  Best Local Similarity   80.7%;  Pred. No. 4.9e-37;
  Matches   88;  Conservative    8;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQKPGQAPRLLIYDASNRATGIP 59
              |||||||| ||| |||||||||||||:| ||:||||||:|||||||||| ||:||||||
Db         21 EIVLTQSPGTLSFSPGERATLSCRASQTVFSSHLAWYQQRPGQAPRLLIYGASSRATGIP 80

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
                ||||||||||||||: |||||||||:|||    |  ||| ||:|:||
Db         81 DRFSGSGSGTDFTLTITRLEPEDFAVYFCQQYGTSPSLTFGGGTRVEIK 129


RESULT 17
KV3K_HUMAN
ID   KV3K_HUMAN     STANDARD;      PRT;   128 AA.
AC   P06311;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region IARC/BL41 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86041852; PubMed=2997711;
RA   Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
RT   "Human immunoglobulin kappa light chain genes of subgroups II and
RT   III.";
RL   Nucleic Acids Res. 13:6499-6513(1985).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z00021; CAA77316.1; -.
DR   PIR; A01899; K3HU41.
DR   HSSP; P01625; 1EEQ.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     20
FT   CHAIN       21    128       Ig kappa chain V-III region IARC/BL41.
FT   DOMAIN      21     43       Framework-1.
FT   DOMAIN      44     54       Complementarity-determining-1.
FT   DOMAIN      55     69       Framework-2.
FT   DOMAIN      70     76       Complementarity-determining-2.
FT   DOMAIN      77    108       Framework-3.
FT   DOMAIN     109    117       Complementarity-determining-3.
FT   DOMAIN     118    128       JK1 segment.
FT   DISULFID    43    108       By similarity.
FT   NON_TER    128    128
SQ   SEQUENCE   128 AA;  14070 MW;  CC8957F0FE3B9012 CRC64;

  Query Match             77.4%;  Score 437.5;  DB 1;  Length 128;
  Best Local Similarity   82.4%;  Pred. No. 1.2e-36;
  Matches   89;  Conservative    5;  Mismatches   13;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              |||||||| |||||||| |||||||||||||| ||||||| ||:||||| |||:|| |||
Db         21 EIVLTQSPGTLSLSPGESATLSCRASQSVSSNLAWYQQKRGQSPRLLIRDASSRANGIPD 80

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||||| || |||||||||||||| |   |:||| |||::||
Db         81 RFSGSGSGTDFTLIISRLEPEDFAVYYCQQYST-SPYTFGQGTKLEIK 127


RESULT 18
KV3A_HUMAN
ID   KV3A_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01619;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig kappa chain V-III region B6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   PubMed=11946339;
RA   Milstein C.;
```

```
RT   "The basic sequences of immunoglobulin kappa chains: sequence studies
RT   of Bence Jones proteins Rad, Fr4 and B6.";
RL   FEBS Lett. 2:301-304(1969).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR   PIR; A01891; K3HUB6.
DR   HSSP; P01625; 1EEQ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin V region.
FT   DISULFID     23     89       By similarity.
FT   NON_TER      108    108
SQ   SEQUENCE   108 AA;  11635 MW;  8BC14FF07A419E3D CRC64;

  Query Match             77.0%;  Score 435;  DB 1;  Length 108;
  Best Local Similarity   77.1%;  Pred. No. 1.8e-36;
  Matches   84;  Conservative   12;  Mismatches   11;  Indels    2;  Gaps    2;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVS-SYLAWYQQKPGQAPRLLIYDASNRATGIP 59
              :||||:|| |||||||:|| ||||||||:| :||||||||||||||:|  |:||||||
Db          1 ZIVLTZSPGTLSLSPGZRAALSCRASQSLSGNYLAWYQQKPGQAPRLLMYGVSSRATGIP 60

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
               |||||||| ||||||| |:||||||||||  :  ||||| |:|::||
Db         61 DRFSGSGSGADFTLTISRLZPEDFAVYYCQQYGS-SPFTFGQGSKLEIK 108


RESULT 19
Q6GMV9
ID   Q6GMV9      PRELIMINARY;      PRT;   235 AA.
AC   Q6GMV9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073793; AAH73793.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   235 AA;  25646 MW;  DF32B580BAD19E4B CRC64;

  Query Match             76.3%;  Score 431;  DB 2;  Length 235;
  Best Local Similarity   81.7%;  Pred. No. 1.2e-35;
  Matches   89;  Conservative    5;  Mismatches   13;  Indels    2;  Gaps    2;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSS-YLAWYQQKPGQAPRLLIYDASNRATGIP 59
              |||||||| |||||||||| |||||||||:| ||||||||||||||||:| || ||||||
Db         21 EIVLTQSPGTLSLSPGERAALSCRASQSVNSKYLAWYQQKPGQAPRLLMYAASIRATGIP 80

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
               |||||||||||||||| || ||||:|:|||     | ||| ||||:||
Db         81 DRFSGSGSGTDFTLTISRLESEDFALYFCQQYGT-SPLTFGGGTKVEIK 128


RESULT 20
KV3G_HUMAN
ID   KV3G_HUMAN     STANDARD;      PRT;   109 AA.
AC   P04206;
DT   20-MAR-1987 (Rel. 04, Created)
DT   20-MAR-1987 (Rel. 04, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-III region GOL (Rheumatoid factor).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=86230578; PubMed=3086710; DOI=10.1016/0161-5890(86)90049-0;
RA   Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
RT   "Amino acid sequence of a light chain variable region of a human
RT   rheumatoid factor of the Wa idiotypic group, in part predicted by its
RT   reactivity with antipeptide antibodies.";
RL   Mol. Immunol. 23:239-244(1986).
DR   PIR; A01893; K3HUGO.
DR   HSSP; P01625; 1EK3.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DISULFID     23     89       By similarity.
FT   NON_TER      109    109
SQ   SEQUENCE   109 AA;  11830 MW;  9349A5B1D93588B6 CRC64;

  Query Match             75.9%;  Score 429;  DB 1;  Length 109;
  Best Local Similarity   80.7%;  Pred. No. 7.5e-36;
  Matches   88;  Conservative    6;  Mismatches   13;  Indels    2;  Gaps    2;

Qy          1 EIVLTQSPATLSLSPGERATLSCRAS-QSVSSYLAWYQQKPGQAPRLLIYDASNRATGIP 59
              |||||||| |||||||||||||||:  |   |||||||||||||||:| ||:||||||
Db          1 EIVLTQSPGTLSLSPGERATLSCRAALLSSRGYLAWYQQKPGQAPRLLMYGASSRATGIP 60

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
               |||||||||||||||| ||||||||||||  :  | :|| ||||:||
Db         61 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS-SPRSFGQGTKVEIK 108
```

```
RESULT 21
KV3J_HUMAN
ID   KV3J_HUMAN     STANDARD;      PRT;   116 AA.
AC   P04434;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region VH precursor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85087932; PubMed=6440122;
RA   Pech M., Zachau H.G.;
RT   "Immunoglobulin genes of different subgroups are interdigitated within
RT   the VK locus.";
RL   Nucleic Acids Res. 12:9229-9236(1984).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X02725; -; NOT_ANNOTATED_CDS.
DR   PIR; A01901; K3HUVH.
DR   HSSP; P01625; 1LVE.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     20
FT   CHAIN       21   >116       Ig kappa chain V-III region VH.
FT   DOMAIN      21     43       Framework-1.
FT   DOMAIN      44     55       Complementarity-determining-1.
FT   DOMAIN      56     70       Framework-2.
FT   DOMAIN      71     77       Complementarity-determining-2.
FT   DOMAIN      78    109       Framework-3.
FT   DOMAIN     110    116       Complementarity-determining-3.
FT   DISULFID    43    109       By similarity.
FT   NON_TER    116    116
SQ   SEQUENCE   116 AA;  12757 MW;  51CD55BA53B21929 CRC64;

  Query Match             74.4%;  Score 420.5;  DB 1;  Length 116;
  Best Local Similarity   87.5%;  Pred. No. 5.9e-35;
  Matches   84;  Conservative    2;  Mismatches    9;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQKPGQAPRLLIYDASNRATGIP 59
              |||:|||| ||||||||| |||||||||| |||| |||||||||||||| || ||| ||
Db         21 EIVMTQSPPTLSLSPGERVTLSCRASQSVSSSYLTWYQQKPGQAPRLLIYGASTRATSIP 80

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWP 95
              ||||||||||||||||||:||||||||||  | |
Db         81 ARFSGSGSGTDFTLTISSLQPEDFAVYYCQQDHNLP 116


RESULT 22
KV3C_HUMAN
ID   KV3C_HUMAN     STANDARD;      PRT;   100 AA.
AC   P01621;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-III region NG9 precursor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84093600; PubMed=6419127;
RA   Bentley D.L.;
RT   "Most kappa immunoglobulin mRNA in human lymphocytes is homologous to
RT   a small family of germ-line V genes.";
RL   Nature 307:77-80(1984).
CC   -!- MISCELLANEOUS: This gene was isolated from the NG9/9.1 hybridoma.
DR   PIR; A01894; K3HUNG.
DR   HSSP; P01625; 1EEQ.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Hybridoma; Immunoglobulin V region; Signal.
FT   NON_TER      1      1
FT   SIGNAL      <1      4
FT   CHAIN        5    100       Ig kappa chain V-III region NG9.
FT   DISULFID    27     93       By similarity.
FT   NON_TER    100    100
SQ   SEQUENCE   100 AA;  10729 MW;  5D9AF363CC52632F CRC64;

  Query Match             73.9%;  Score 417.5;  DB 1;  Length 100;
  Best Local Similarity   89.4%;  Pred. No. 1e-34;
  Matches   84;  Conservative    2;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQKPGQAPRLLIYDASNRATGIP 59
              |||||||| |||||||||||||||||||| |||||||||||||||||| |::||||||
Db          5 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGATSRATGIP 64

Qy         60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSN 93
              ||||| |||||||||| |||||||||||||  |
Db         65 DRFSGSASGTDFTLTISRLEPEDFAVYYCQQYGN 98


RESULT 23
Q6GMX8
ID   Q6GMX8      PRELIMINARY;      PRT;   236 AA.
AC   Q6GMX8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
```

```
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Primary B-Cells;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073764; AAH73764.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25707 MW;  4FC8E14B6559EFC9 CRC64;

  Query Match            73.9%;  Score 417.5;  DB 2;  Length 236;
  Best Local Similarity   71.3%;  Pred. No. 2.7e-34;
  Matches   77;  Conservative   19;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              :| :||||:::| | |:| |::||||| :||:||||||||:||:|||| ||:  :|:|:
Db         23 DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPS 82

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              ||||||||||||||||:||||| ||||| :: |||||||||||||
Db         83 RFSGSGSGTDFTLTISSLQPEDFATYYCQQAHSF-PFTFGPGTKVDIK 129


RESULT 24
KV1M_HUMAN
ID   KV1M_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01605;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-I region Lay.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77038198; PubMed=824717;
RA   Capra J.D., Klapper D.G.;
RT   "Complete amino acid sequence of the variable domains of two human IgM
RT   anti-gamma globulins (Lay/Pom) with shared idiotypic specificities.";
RL   Scand. J. Immunol. 5:677-684(1976).
CC   -!- MISCELLANEOUS: The second and third hypervariable regions of this
CC       chain are identical with those of the human POM V-III kappa chain,
CC       with which it shares certain idiotypic determinants.
CC   -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC       globulin activity.
DR   PIR; A01871; K1HULY.
DR   HSSP; P01607; 1BWW.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin V region.
FT   DOMAIN       1     23       Framework-1.
FT   DOMAIN      24     34       Complementarity-determining-1.
FT   DOMAIN      35     49       Framework-2.
FT   DOMAIN      50     56       Complementarity-determining-2.
FT   DOMAIN      57     88       Framework-3.
FT   DOMAIN      89     97       Complementarity-determining-3.
FT   DOMAIN      98    107       Framework-4.
FT   DISULFID    23     88       By similarity.
FT   NON_TER    108    108
SQ   SEQUENCE   108 AA;  11834 MW;  739993A95431434A CRC64;

  Query Match            72.7%;  Score 410.5;  DB 1;  Length 108;
  Best Local Similarity   68.5%;  Pred. No. 5.7e-34;
  Matches   74;  Conservative   19;  Mismatches   14;  Indels    1;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              :| :||||::||:| |:| |::|:|||:|::|| ||||||| ||:|||| || |  |:|:
Db          1 DIQMTQSPSSLSVSVGDRVTITCQASQNVNAYLNWYQQKPGLAPKLLIYGASTREAGVPS 60

Qy         61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
              |||||||||||| |||||:||| | ||||| :|||| ||| ||||::|
Db         61 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYNNWPP-TFGQGTKVEVK 107


RESULT 25
KV1D_HUMAN
ID   KV1D_HUMAN     STANDARD;      PRT;   107 AA.
AC   P01596;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Ig kappa chain V-I region CAR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75075135; PubMed=4216454;
RA   Milstein C.P., Deverson E.V.;
RT   "Primary structure of kappa light chain from a human myeloma
RT   protein.";
RL   Eur. J. Biochem. 49:377-391(1974).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC       marker.
CC   -!- MISCELLANEOUS: This chain was isolated from a myeloma protein.
DR   PIR; A01864; K1HUAR.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Glycoprotein; Immunoglobulin V region.
FT   CARBOHYD     28     28       N-linked (GlcNAc. . .).
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11703 MW;  E1BF0DF9844C3346 CRC64;

  Query Match            71.5%;  Score 404;  DB 1;  Length 107;
  Best Local Similarity   67.6%;  Pred. No. 2.6e-33;
  Matches   73;  Conservative   22;  Mismatches   11;  Indels    2;  Gaps    1;

Qy          1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
              :| :||||:||| | |:|  ::|||||::||:|||||||||:||::||| :|:  :|:|:
Db          1 DIQMTQSPSTLSASVGDRVAITCRASQNISSWLAWYQQKPGKAPKVLIYKSSSLESGVPS 60
```

```
Qy          61 RFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
               ||||||||||||||||||:|::|| ||||| : :  ||||||||||||
Db          61 RFSGSGSGTDFTLTISSLZPBBFATYYCQQYNTF--FTFGPGTKVDIK 106
```

Search completed: June 16, 2005, 07:38:56
Job time : 109.484 secs